

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OK protein - protein search, using sw model

Run on: July 15, 2003, 07:15:55 ; Search time 41 Seconds
(without alignments)
801.902 Million cell updates/sec

Title: US-09-940-063-2
Perfect score: 1794
Sequence: 1 MAEHYHEDYGFSSFNDSQ.....DNKTFSSHVTEATSMFQL 342

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Reached: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR-73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	619	34.5	369	2	JC5068
2	608.5	33.9	378	2	B55735
3	608.5	33.9	378	2	A55735
4	588.5	32.8	378	2	A45680
5	568	31.7	350	2	JN0621
6	524.5	29.2	352	2	A45747
7	521.5	29.1	374	2	I38450
8	520.5	29.0	360	2	JC2443
9	516	28.8	353	2	S28787
10	512.5	28.6	355	2	A45177
11	508.5	28.3	352	2	G00048
12	508	28.3	359	2	A48921
13	507.5	28.3	359	2	A53752
14	505.5	28.2	360	2	A57160
15	505	28.1	355	2	J01231
16	498.5	27.8	359	2	I49341
17	497.5	27.6	367	2	J60349
18	495.5	27.6	355	2	G02436
19	494	27.5	352	2	A43113
20	491.5	27.4	383	2	S55594
21	490	27.3	360	2	A53611
22	489	27.3	360	2	UC4587
23	484	27.0	356	2	S42096
24	484	27.0	359	2	S15403
25	481	26.8	359	2	JC1104
26	478	26.6	359	2	A48857
27	477	26.6	359	2	S44425
28	476.5	26.6	350	2	A39445
29	476.5	26.6	355	2	I49339

30	474	26.4	359	2	A42656	angiotensin II rec
31	469	26.1	356	2	I49340	MRP-1 alpha recept
32	467	26.0	359	2	JC2134	angiotensin II rec
33	465.5	25.9	355	2	JC5067	G protein-coupled
34	465	25.9	359	2	I39418	angiotensin II rec
35	465	25.9	359	2	JH0621	angiotensin II rec
36	458	25.5	359	2	JC1194	angiotensin II rec
37	458	25.5	359	2	J01516	angiotensin II rec
38	447	24.9	355	2	JC4304	orphan G protein-c
39	444	24.7	374	2	S32785	G protein-coupled
40	442	24.6	359	2	I51372	angiotensin II rec
41	439.5	24.5	354	2	I58186	probable G protein
42	429	23.9	372	2	S26667	G protein-coupled
43	427.5	23.8	354	2	A23669	interleukin-8 rece
44	426.5	23.8	374	2	S42638	G protein-coupled
45	426	23.7	327	2	S56162	MDR1s protein - h

ALIGNMENTS

RESULT 1

JC5068
G:protein-coupled receptor CKR-L3 - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C:Accession: JC5068
R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-11k
A:Reference number: JC5067; MUID:97040707; PMID:8886020
A:Accession: JC5068
A:Molecule type: DNA
A:Residues: 1-369 <ZAB>
A:Cross-references: EXBL:Z79784; NID:91668737; PIDN:CA802144.1; PID:91668738
C:Comment: This protein belongs to the family of alpha chemokine receptors.
C:Genetics:
A:Gene: GDB:CMKR6; STRL22; GPR29; CCR6; CKR-L3; GPR-CY4
A:Cross-references: GDB:5370639; OMIM:601835
A:Map position: 6q27-6q27
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:42-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:160-180/Domain: transmembrane #status predicted <TM4>
F:212-233/Domain: transmembrane #status predicted <TM5>
F:250-271/Domain: transmembrane #status predicted <TM6>
F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match	34.5%	Score 619;	DB 2;	Length 369;
Best local similarity	36.3%	Pred. No. 1.3e-42;		
Matches 135;	Conservative	77;	Mismatches 116;	Indels 44;
			Gaps	9;
QY	5	DYHEDYGFSSFNDSOEHDPL-----QFSKVLPCMYLVFVGLGNSLVIVIS	56	
DB	8	DSSEDDY-FVSVNTSVYSVDSEMLCSIQEVNQFRLFPALVSLVCGILGNLVITFE	66	
QY	57	IFYHKLQSLDVEFLVNLPLADLVVCTLPFAVA-GIHEVFGOMCKSLGITTYNT	115	
DB	67	AFYKRSMTDVIYLLNMAIDILEVLTPFAVSHAGCAWFSNATCLGIYAINEFC	126	
QY	116	SMILITCTVDRFLVAVKATFAYNOAKRMWGVTSLIIVISLVSLPQIIVGNFL	175	
DB	127	GMLITCTSMDRYIAIVQATSFRLRSITICILVAVGLSVIISSTFVFNQKNT	186	
QY	176	D-KLIGYHDEAIS-----TVVLATQMTLGFPLPLTMIVCYSVIITLLHAGFOKRR	228	
DB	187	QGSVCEPKYQTVSEPIRMKLMGLGELLFEPFLPMFCYFIVKTLVQAQNSRHK	246	
QY	229	SKLIIFLVMAVFLTLQMFNLM-----KFLRSHWEYVAMTSRHYITMVEALAYL	279	
DB	247	AIRVIAIVVLEFLACQIPHNVLLVLTANLCKMNRSCQSE---KLIGYKTVVEVLAFL	302	

QY 280 RACINPVYIAYVSLKFRNKIVADICCLPLGVSHOMKS-----SEDSKTS 330
Db 303 HCCINPVYIAYIGOKFRNFKILKDLWC-----VRRYKSSGFCAGRYSENISRQSE 357
QY 331 SHNVEATSMFOL 342
Db 358 TADNDNASSFTW 369

RESULT 2

B55735

Lymphocyte-specific G protein-coupled receptor EB11 - human

N.Altreanate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1

C:Species: Homo sapiens (man)

C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000

C:Accession: B55735; S52443

R:Schweickart, V.L.; Raport, C.J.; Godtska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.

Genomics 23, 643-650, 1994

A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor

A:Reference number: A55735; MUID:95154835; PMID:7851893

A:Accession: B55735

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-378 <SCH>

A:Cross-references: GB:L31581; NID:9468319; PIDN:AAA74231.1; PID:9468320

R:Burgstahler, R.; Kempkes, B.; Staude, K.; Lipp, M.

Submitted to the EMBL Data Library, February 1995.

A:Description: The expression of the chemokine receptor BUR2/EB11 is specifically trans

A:Reference number: S52443

A:Accession: S52443

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 21-378 <BUR>

A:Cross-references: EMBL:X84702

C:Genetics:

A:Gene: GDB:CMKBR7; EB11; BLR2; CCR7

A:Cross-references: GDB:342065; OMIM:600242

A:Map position: 17q12-17q21.2

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

Query Match 33.9%; Score 608.5; DB 2; Length 378;
Best Local Similarity 36.9%; Pred. No. 9.1e-42;

Matches 122; Conservative 84; Mismatches 106; Indels 19; Gaps 8;

QY 24 QDLQFSKVPFLPCMYLVFVCGLVGNSLVVISIFYHKLQSLDVFVNLPLADLVFVCT 83
Db 51 KDVNFKAMFLPIMYSIICFVGLGNGLVLYIYFRKLTMTDTYLLNLAVADILFLLT 110
84 LPEAVAGIHFWVGVGWCKSLGITYINFTSMILCTIVDRFIYVVKATKAYNOAK 143
Db 111 LPEAVAGIAKSWGVGHECKIFAIYKMSFSGMLLCISIDRYVAIVQVSAHRHRAR 170
144 RMTGKVTSLIWIYSLVSPQIYGNV---FNLDKLICY---HDEAISTVLANQMT 197
Db 171 VLISKISCGVIMLAVLSIPELLYSDLRSSSEQAMRCSLITEHFAFTIOVA-QMV 229
QY 198 LGFLLPLMTIVCYSVIITKLLHAGGFQKHSRLKIIFLVMAVFLLTQMPN-----LM 250
Db 230 IGFVLPPLAMSFCLYIIRTLQARNFERNKAKIVIAVVVFVIFQDLPYGVVLAQTV 289
QY 251 KF-IRSTHWEYVAMTSFHYITMTYEAIALACINPVYIAYVSLKFRNKIVADICCL 309
Db 290 NFNTSTSCVSLKQNLNAYD--VYISLACVRCVNPFLYAFIGVFRNDLFLKFKDGL 347
QY 310 PYLGVSHOMKSSEDSKTSFASHNVEATSMF 340
Db 348 SQEOL-RQWSSCR-HIRSSMSVAETTTTF 376

RESULT 3

A55735

G protein-coupled receptor EB11 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
C:Accession: A55735
R:Schweickart, V.L.; Raport, C.J.; Godtska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T

Genomics 23, 643-650, 1994

A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled recep

A:Reference number: A55735; MUID:95154835; PMID:7851893

A:Accession: A55735

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-378 <SCH>

A:Cross-references: GB:L31580; NID:9468340; PIDN:AAA74232.1; PID:9468341

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

Query Match 33.9%; Score 608.5; DB 2; Length 378;
Best Local Similarity 36.3%; Pred. No. 9.1e-42;

Matches 120; Conservative 84; Mismatches 108; Indels 19; Gaps 8;

QY 24 QDLQFSKVPFLPCMYLVFVCGLVGNSLVVISIFYHKLQSLDVFVNLPLADLVFVCT 83
Db 51 KDVNFKAMFLPIMYSIICFVGLGNGLVLYIYFRKLTMTDTYLLNLAVADILFLLT 110
QY 84 LPEAVAGIHFWVGVGWCKSLGITYINFTSMILCTIVDRFIYVVKATKAYNOAK 143
Db 111 LPEAVAGIAKSWGVGHECKIFAIYKMSFSGMLLCISIDRYVAIVQVSAHRHRAR 170
QY 144 RMTGKVTSLIWIYSLVSPQIYGNV---FNLDKLICY---HDEAISTVLANQMT 197
Db 171 VLISKISCGVIMLAVLSIPELLYSDLRSSSEQAMRCSLITEHFAFTIOVA-QMV 229
QY 198 LGFLLPLMTIVCYSVIITKLLHAGGFQKHSRLKIIFLVMAVFLLTQMPN-----LM 250
Db 230 IGFVLPPLAMSFCLYIIRTLQARNFERNKAKIVIAVVVFVIFQDLPYGVVLAQTV 289
QY 251 KF-IRSTHWEYVAMTSFHYITMTYEAIALACINPVYIAYVSLKFRNKIVADICCL 309
Db 290 NFNTSTSCVSLKQNLNAYD--VYISLACVRCVNPFLYAFIGVFRNDLFLKFKDGL 347
QY 310 PYLGVSHOMKSSEDSKTSFASHNVEATSMF 340
Db 348 SQEOLRH-WSSCR-HVNRASVMEATTTTF 376

RESULT 4
A55680
G protein-coupled peptide receptor EBI 1 - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C:Accession: A45680
R:Bitkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A:Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-couple
A:Reference number: A45680; MUID:93186173; PMID:8383238
A:Accession: A45680
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-378 <BIR>
A:Cross-references: GB:L08176; NID:9183484; PID:9183485
A:Note: sequence extracted from NCBI backbone (NCBI:127094, NCBI:127095)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 32.8%; Score 588.5; DB 2; Length 378;
Best Local Similarity 36.3%; Pred. No. 3.7e-40;
Matches 120; Conservative 84; Mismatches 108; Indels 19; Gaps 8;

QY 24 QDLQFSKVPFLPCMYLVFVCGLVGNSLVVISIFYHKLQSLDVFVNLPLADLVFVCT 83
Db 51 KDVNFKAMFLPIMYSIICFVGLGNGLVLYIYFRKLTMTDTYLLNLAVADILFLLT 110

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2003, 07:02:50 ; Search time 23 Seconds
(without alignments)
616.735 Million cell updates/sec

Title: US-09-940-063-2
Perfect score: 1794
Sequence: 1 MAEHYHEDYGFSSFNDSQ.....DNKTFASHNEATSMFQL 342

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 112892
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1794	100.0	342	1 CCR6_HUMAN	O00574 homo sapien
2	1730	96.4	342	1 CCR6_MACNE	O19024 macaca neme
3	1717	95.7	342	1 CCR6_CERAE	O18983 cercopithe
4	1702.5	94.9	343	1 CCR6_MACMU	Q9X145 macaca mula
5	619	34.5	374	1 CCR6_HUMAN	P16864 homo sapien
6	612	34.1	357	1 CCR6_HUMAN	P16864 homo sapien
7	608.5	33.9	378	1 CCR7_HUMAN	P22248 homo sapien
8	608.5	33.9	378	1 CCR7_HUMAN	P22248 homo sapien
9	608	33.9	369	1 CCR9_MOUSE	P47774 mus musculu
10	598.5	33.4	369	1 CCR9_MOUSE	Q9WU74 mus musculu
11	568	31.7	350	1 CCR6_MOUSE	O54689 mus musculu
12	560	31.2	350	1 CCR6_MOUSE	P53350 bos taurus
13	524.5	29.2	352	1 CCR4_HUMAN	G9NP89 homo sapien
14	524	29.2	353	1 CCR4_HUMAN	P30991 homo sapien
15	521.5	29.1	349	1 CCR4_FELCA	P56498 felis silve
16	521.5	29.1	360	1 CCR2_MACMU	O08565 rattus norv
17	521.5	29.1	374	1 CCR2_HUMAN	O18793 macaca mula
18	516	28.8	353	1 CCR4_BOVIN	P41597 homo sapien
19	515.5	28.7	352	1 CCR4_PAPAN	P56491 papio anubi
20	514.5	28.6	352	1 CCR4_MACMU	P79394 macaca mula
21	512.5	28.7	355	1 CCR1_HUMAN	P32246 homo sapien
22	511.5	28.5	352	1 CCR4_CERTO	O62747 cercocobus
23	510	28.4	359	1 CCR4_MOUSE	P70658 m.c-x-c che
24	509	28.4	373	1 CCR2_RAT	O55193 rattus norv
25	508.5	28.3	352	1 CCR4_MACFA	Q28474 macaca fasc
26	508.5	28.3	354	1 CCR5_RAT	O08556 rattus norv
27	508	28.3	359	1 IL8B_MOUSE	P53343 mus musculu
28	508	28.3	373	1 CCR2_MOUSE	P51683 mus musculu
29	507.5	28.2	358	1 IL8B_RABIT	P53344 oryctolagus
30	505.5	28.3	360	1 CCR4_HUMAN	P51679 homo sapien
31	505	28.1	355	1 IL8A_HUMAN	P21109 oryctolagus
32	503.5	28.1	356	1 IL8B_CANFA	O97571 canis famli
33	502	28.0	368	1 CCR3_HUMAN	P49682 homo sapien

34	500	27.9	359	1 CCR3_RAT	O54814 rattus norv
35	499.5	27.8	355	1 CCR3_CERAE	P56492 cercopithe
36	498.5	27.8	355	1 CCR3_HUMAN	P51679 homo sapien
37	497.5	27.7	367	1 CCR3_MOUSE	O08410 mus musculu
38	497	27.7	352	1 CCR5_CERAE	P56493 cercopithe
39	496	27.6	352	1 CCR5_HYLL	O97883 hylobates 1
40	495.5	27.6	355	1 CCR3_MACMU	P56483 macaca mula
41	494	27.5	352	1 CCR5_GORGO	P56439 gorilla gor
42	494	27.5	352	1 CCR5_HUMAN	P51681 homo sapien
43	493.5	27.5	352	1 CCR3_MOUSE	P51678 mus musculu
44	493	27.5	352	1 CCR5_TRAFR	O97878 trachypithe
45	492.5	27.5	358	1 CCR3_CAVVO	Q92213 cavia porce

ALIGNMENTS

```

RESULT 1
ID CCR6_HUMAN STANDARD: PRT: 342 AA.
AC O00574: 000575:
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-X-C chemokine receptor type 6 (CXCR-6) (G protein-coupled
DE receptor bonzo) (G protein-coupled receptor STRL33).
GN CXCR6 OR BONZO OR STRL33 OR TYMSR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97373958; PubMed=9230441;
RA Deng H.K., Unutmaz D., KewalRamani V.N., Littman D.R.;
RT "Expression cloning of new receptors used by simian and human
RT immunodeficiency viruses."
RL Nature 388:296-300(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97311099; PubMed=9166430;
RA Lao F., Alkhatib G., Peden K.W.C., Sharma G., Berger E.A.,
RA Farber J.M.;
RT "STRL33, A novel chemokine receptor-like protein, functions as a
RT fusion cofactor for both macrophage-tropic and T cell line-tropic
RT HIV-1."
RL J. Exp. Med. 185:2015-2023(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97431687; PubMed=9285716;
RA Loetscher M., Amara A., Oberlin E., Brass N., Legler D.F.,
RA Loetscher P., Arenzana-Seisdedos F., Moser B.;
RT "TYMSR, a putative chemokine receptor selectively expressed in
RT activated T cells, exhibits HIV-1 coreceptor function."
RL Curr. Biol. 7:652-660(1997).
CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE CXCL16. USED AS A
CC CORECEPTOR BY SIVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LYMPHOID TISSUES AND ACTIVATED T
CC CELLS.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to: license@isb-sib.ch).
CC -----
CC EMBL: AF007545; AAB64221.1; -

```

```

DR EMBL: U73529; AAB61456.1; -
DR EMBL: U73531; AAB61457.1; -
DR EMBL: Y13248; CAA73698.1; -
DR MIM: 605163; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_RHODOPS.
DR PROSITE: PS00237; G-PROTEIN_REC_P1.1; 1.
DR PROSITE: PS0262; G-PROTEIN_REC_P2.1; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
FT DOMAIN 1 32
FT TRANSSEM 33 59
FT DOMAIN 60 68
FT TRANSSEM 69 89
FT DOMAIN 90 103
FT TRANSSEM 104 125
FT DOMAIN 126 143
FT TRANSSEM 144 164
FT DOMAIN 165 187
FT TRANSSEM 188 215
FT DOMAIN 216 231
FT TRANSSEM 232 259
FT DOMAIN 260 275
FT TRANSSEM 276 293
FT DOMAIN 294 342
FT DISULFID 102 180
FT CARBOHYD 16 16
FT VARIANT 25 25
FT D->A (IN STRL33.3).
/ftid-VAR.003506.
SQ SEQUENCE 342 AA; 39280 MM; 9FBC02556D1082E CRC64;

Query Match 100.0%; Score 1794; DB 1; Length 342;
Best Local Similarity 100.0%; Pred. No. 8.1e-95;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEHYEDYGEFFSFFNSOEHODFLOFSEKVFPCMYLVFVCGVGNLSLVYISFYH 60
DB 1 MAEHYEDYGEFFSFFNSOEHODFLOFSEKVFPCMYLVFVCGVGNLSLVYISFYH 60
QY 61 KLOSLDVLFLVNLPLADLVFVCTLPFWAYAGIHEWFGQWCKSLGITYINFTSMIL 120
DB 61 KLOSLDVLFLVNLPLADLVFVCTLPFWAYAGIHEWFGQWCKSLGITYINFTSMIL 120
QY 121 TCITVDREFIYVAVKATKAYNOQAKRMWGKYSLLIWIYISLVSPQIITGVNFDLILC 180
DB 121 TCITVDREFIYVAVKATKAYNOQAKRMWGKYSLLIWIYISLVSPQIITGVNFDLILC 180
QY 181 GYHDEAISTVVLATQMTLGFELPLMTIYCVSVIITKLLHAGGFQKRSIKIIFLVAVF 240
DB 181 GYHDEAISTVVLATQMTLGFELPLMTIYCVSVIITKLLHAGGFQKRSIKIIFLVAVF 240
QY 241 LTQMPENLKKFIRSTHWEYVAMTSFHYITMVEALAYLRACINPVLVAFVSLKFRKNF 300
DB 241 LTQMPENLKKFIRSTHWEYVAMTSFHYITMVEALAYLRACINPVLVAFVSLKFRKNF 300
QY 301 KLVKDIGCLPYLGVSHQWKSSEDSKTFSSASHNVEATSMFQL 342
DB 301 KLVKDIGCLPYLGVSHQWKSSEDSKTFSSASHNVEATSMFQL 342
DB 301 KLVKDIGCLPYLGVSHQWKSSEDSKTFSSASHNVEATSMFQL 342

RESULT 2
CCR6_MACNE
ID CCR6_MACNE STANDARD; PRT; 342 AA.
AC 019024;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-X-C chemokine receptor type 6 (CXCR-6) (CXCR-6) (G protein-coupled
DE receptor bonzo).
GN CXCR6 OR BONZO.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

```

```

OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97373958; PubMed=9230441;
RA Deng H.K., Unutmaz D., Kewallramani V.N., Littman D.R.;
RT "Expression cloning of new receptors used by simian and human
RT immunodeficiency viruses."
RL Nature 388:296-300(1997).
CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE CXCL6. USED AS A
CC CORECEPTOR BY STVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF007858; AAB64224.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_RHODOPS.
DR PROSITE: PS00237; G-PROTEIN_REC_P1.1; 1.
DR PROSITE: PS0262; G-PROTEIN_REC_P2.1; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 32
FT TRANSSEM 33 59
FT DOMAIN 60 68
FT TRANSSEM 69 89
FT DOMAIN 90 103
FT TRANSSEM 104 125
FT DOMAIN 126 143
FT TRANSSEM 144 164
FT DOMAIN 165 187
FT TRANSSEM 188 215
FT DOMAIN 216 231
FT TRANSSEM 232 259
FT DOMAIN 260 275
FT TRANSSEM 276 293
FT DOMAIN 294 342
FT DISULFID 102 180
FT CARBOHYD 16 16
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 342 AA; 39297 MM; 55F9F68CB62D2D5 CRC64;

Query Match 96.4%; Score 1730; DB 1; Length 342;
Best Local Similarity 95.6%; Pred. No. 3.2e-91;
Matches 327; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAEHYEDYGEFFSFFNSOEHODFLOFSEKVFPCMYLVFVCGVGNLSLVYISFYH 60
DB 1 MAEHYEDYGEFFSFFNSOEHODFLOFSEKVFPCMYLVFVCGVGNLSLVYISFYH 60
QY 61 KLOSLDVLFLVNLPLADLVFVCTLPFWAYAGIHEWFGQWCKSLGITYINFTSMIL 120
DB 61 KLOSLDVLFLVNLPLADLVFVCTLPFWAYAGIHEWFGQWCKSLGITYINFTSMIL 120
QY 121 TCITVDREFIYVAVKATKAYNOQAKRMWGKYSLLIWIYISLVSPQIITGVNFDLILC 180
DB 121 TCITVDREFIYVAVKATKAYNOQAKRMWGKYSLLIWIYISLVSPQIITGVNFDLILC 180
QY 181 GYHDEAISTVVLATQMTLGFELPLMTIYCVSVIITKLLHAGGFQKRSIKIIFLVAVF 240
DB 181 GYHDEAISTVVLATQMTLGFELPLMTIYCVSVIITKLLHAGGFQKRSIKIIFLVAVF 240
QY 241 LTQMPENLKKFIRSTHWEYVAMTSFHYITMVEALAYLRACINPVLVAFVSLKFRKNF 300
DB 241 LTQMPENLKKFIRSTHWEYVAMTSFHYITMVEALAYLRACINPVLVAFVSLKFRKNF 300
QY 301 KLVKDIGCLPYLGVSHQWKSSEDSKTFSSASHNVEATSMFQL 342
DB 301 KLVKDIGCLPYLGVSHQWKSSEDSKTFSSASHNVEATSMFQL 342

```

Db 301 KLVADICLPYLGVSQWKSSEDSKTFSSASHNEATSMFOL 342

RESULT 3

ID	CCR6_CERAE	STANDARD	PRT	342 AA
AC	018983			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	C-X-C chemokine receptor type 6 (CXCR-6) (G protein-coupled receptor bonzo).			
DE	receptor bonzo).			
GN	CXCR6 OR BONZO.			
OS	Cercopithecus aethiops (Green monkey) (Grivet).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
OC	Cercopithecinae; Cercopithecus.			
NCBI	taxid:9534;			
[1]				
SEQUENCE FROM N.A.				
RA	MEDLINE=97373958; PubMed=9230441;			
RA	Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;			
RT	"Expression cloning of new receptors used by simian and human			
RT	immunodeficiency viruses."			
RL	Nature 388:296-300(1997).			
CC	-1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE CXCL6. USED AS A			
CC	CORECEPTOR BY SVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AF007859; AAB64225.1;			
DR	InterPro: IPR000276; GPCR_Rhodopsn.			
DR	Pfam: PF00001; 7tm.1.1.			
DR	PRINTS; PR00237; GPCR_Rhodopsn.			
DR	PROSITE; PS00237; G-PROTEIN_RECPEP_FL_1; 1.			
DR	PROSITE; PS50262; G-PROTEIN_RECPEP_FL_2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.			
FT	DOMAIN 1			
FT	TRANSMEM 33			
FT	DOMAIN 60			
FT	TRANSMEM 69			
FT	DOMAIN 90			
FT	TRANSMEM 103			
FT	DOMAIN 104			
FT	TRANSMEM 126			
FT	DOMAIN 143			
FT	TRANSMEM 144			
FT	DOMAIN 165			
FT	TRANSMEM 187			
FT	DOMAIN 188			
FT	TRANSMEM 215			
FT	DOMAIN 216			
FT	TRANSMEM 232			
FT	DOMAIN 259			
FT	TRANSMEM 260			
FT	DOMAIN 275			
FT	TRANSMEM 293			
FT	DOMAIN 342			
FT	DISULFID 102			
FT	CARBOHYD 16			
FT	SEQUENCE 342 AA; 39226 MW; 6CBFE38965E919E CRC64;			
SO	SEQUENCE			
Qy	1 MAEHYEDYGFSSFNDSOEHODFLQFSKVFPCMTLVFVCGLVGNSLVLSIFVH 60			
Db	1 MAEYDHDNDFNFSNDSOEHODFLQFSKVFPCMTLVFVCGLVGNSLVLSIFVH 60			
Query Match	95.7%; Score 1717; DB 1; Length 342;			
Best Local Similarity	95.3%; Pred. No. 1.7e-90;			
Matches 326; Conservative 9; Mismatches 7; Indels 0; Gaps 0;				

Qy 61 KLSLTDFVLNPLADLVEYCTLPENAVAGIHEWFGQVCKSLGIYTIINFTSMIL 120

Db 61 KLSLTDFVLNPLADLVEYCTLPENAVAGIHEWFGQVCKSLGIYTIINFTSMIL 120

Qy 121 TCITVDREIVVVKATKAVNOAKRMWGKYSLLIWIISLVSPQIITGVNFDLILC 180

Db 121 TCITVDREIVVVKATKAVNOAKRMWGKYSLLIWIISLVSPQIITGVNFDLILC 180

Qy 181 GYHDEAISTVYLAQMTLGFPLPLTMIVCSVITIKTLHAGGFQKRSKLIIFLVAVF 240

Db 181 GYHDEAISTVYLAQMTLGFPLPLTMIVCSVITIKTLHAGGFQKRSKLIIFLVAVF 240

Qy 241 LTQMPENLKFIRSTHEEYVAMTSFEYTIIVTEAIVLACNLPVLAFAVSLKRRNFV 300

Db 241 LTQMPENLKFIRSTHEEYVAMTSFEYTIIVTEAIVLACNLPVLAFAVSLKRRNFV 300

Qy 301 KLVADICLPYLGVSQWKSSEDSKTFSSASHNEATSMFOL 342

Db 301 KLVADICLPYLGVSQWKSSEDSKTFSSASHNEATSMFOL 342

RESULT 4

ID	CCR6_MACMU	STANDARD	PRT	343 AA
AC	09XT45			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	C-X-C chemokine receptor type 6 (CXCR-6) (G protein-coupled receptor bonzo) (G protein-coupled receptor STRL3).			
DE	receptor bonzo) (G protein-coupled receptor STRL3).			
GN	CXCR6 OR BONZO OR STRL3.			
OS	Macaca mulatta (Rhesus macaque).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
OC	Cercopithecinae; Macaca.			
NCBI	taxid:9544;			
[1]				
SEQUENCE FROM N.A.				
RA	MEDLINE=21354176; PubMed=11461684;			
RA	Margulies B.J., Hauer D.A., Clements J.E.;			
RT	"Identification and comparison of eleven rhesus macaque chemokine			
RT	receptors."			
RL	AIDS Res. Hum. Retroviruses 17:981-986(2001).			
CC	-1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE CXCL6. USED AS A			
CC	CORECEPTOR BY SVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AF124380; AAD31419.1;			
DR	InterPro: IPR000276; GPCR_Rhodopsn.			
DR	Pfam: PF00001; 7tm.1.1.			
DR	PRINTS; PR00237; GPCR_Rhodopsn.			
DR	PROSITE; PS00237; G-PROTEIN_RECPEP_FL_1; 1.			
DR	PROSITE; PS50262; G-PROTEIN_RECPEP_FL_2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.			
FT	DOMAIN 1			
FT	TRANSMEM 33			
FT	DOMAIN 61			
FT	TRANSMEM 69			
FT	DOMAIN 70			
FT	TRANSMEM 91			
FT	DOMAIN 105			
FT	TRANSMEM 126			
FT	DOMAIN 127			
FT	TRANSMEM 144			
FT	DOMAIN 145			
FT	TRANSMEM 166			
FT	DOMAIN 189			
FT	TRANSMEM 216			
Qy	1 MAEYDHDNDFNFSNDSOEHODFLQFSKVFPCMTLVFVCGLVGNSLVLSIFVH 60			
Db	1 MAEYDHDNDFNFSNDSOEHODFLQFSKVFPCMTLVFVCGLVGNSLVLSIFVH 60			
Query Match	95.7%; Score 1717; DB 1; Length 342;			
Best Local Similarity	95.3%; Pred. No. 1.7e-90;			
Matches 326; Conservative 9; Mismatches 7; Indels 0; Gaps 0;				

FT DOMAIN 217 232 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 233 260 6 (POTENTIAL).
 FT DOMAIN 261 276 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 277 294 7 (POTENTIAL).
 FT DOMAIN 295 343 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 17 17 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 103 181 BY SIMILARITY.
 SQ SEQUENCE 343 AA; 39423 MW; 48DB2544949EB83F CRC64;
 Query Match 94.9%; Score 1702.5; DB 1; Length 343;
 Best Local Similarity 94.8%; Pred. No. 1,le-89;
 Matches 325; Conservative 9; Mismatches 8; Indels 1; Gaps 1;
 QY 1 MAEDYEDYDGF-SSEFSSDSEEDDLOSKYFLPMYLVYVYCGVGSVLYVIFY 59
 DB 1 MAEDYHEDDGFSLFSSDSEEDDLOSKYFLPMYLVYVYCGVGSVLYVIFY 60
 QY 60 HKLOSLDVEFLVNLPLDLVFCVCTLPWYAGHIEWGVGOMCKSLGITYNTYMLI 119
 DB 61 HKLOSLDVEFLVNLPLDLVFCVCTLPWYAGHIEWGVGOMCKSLGITYNTYMLI 120
 QY 120 LFCITVDREFLVYVYKATKAYNOAKRMVGTSLIWIWISLVSLPQIIGVFNLDKLI 179
 DB 121 LFCITVDREFLVYVYKATKAYNOAKRMVGTSLIWIWISLVSLPQIIGVFNLDKLI 180
 QY 180 CGYHDEAISTVYVATQMTLGFPLPLMYCYVITYITLLHAGCFQKHSIKITFLVAV 239
 DB 181 CGYHDEAISTVYVATQMTLGFPLPLMYCYVITYITLLHAGCFQKHSIKITFLVAV 240
 QY 240 FLITVDREFLVYVYKATKAYNOAKRMVGTSLIWIWISLVSLPQIIGVFNLDKLI 299
 DB 241 FLITVDREFLVYVYKATKAYNOAKRMVGTSLIWIWISLVSLPQIIGVFNLDKLI 300
 QY 300 WKLVKIDICLPYLVGVSHQMSSEDSNKTFSASHNVEATSMFOL 342
 DB 301 WKLVKIDICLPYLVGVSHQMSSEDSNKTFSASHNVEATSMFOL 343

RESULT 5
 CKR6_HUMAN STANDARD; PRT; 374 AA.
 AC P51684; Q92846; P78553;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 6 (C-C CKR-6) (CC-CKR-6) (LARC receptor) (GPR-CY4) (GPRCY4) (Chemokine receptor-like 3) (CKR-L3) (DRY6).
 GN CCR6 OR CKR6 OR STRL22 OR GPR29 OR CKRL3.
 OC Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND FUNCTION.
 RX MEDLINE=97313465; PubMed=9169459;
 RA Bbba M., Imei T., Nishimura M., Kakizaki M., Takagi S., Hieshima K., Nomiyaama H., Yoshie O.;
 RT "Identification of CCR6, the specific receptor for a novel lymphocyte-directed CC chemokine LARC";
 RT J. Biol. Chem. 272:14893-14898(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Lautens L.L., Modi W., Bonner T.I.;
 RL Submitted (APR-1996) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97040707; PubMed=8886020;
 RA Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;
 RT "Molecular cloning and RNA expression of two new human chemokine receptor-like genes";
 RT Biochem. Res. Commun. 227:846-853(1996).
 RN [4]

RP SEQUENCE FROM N.A.
 RA McCoy R., Perlmuter D.H.;
 RL Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97224503; PubMed=9070937;
 RA Liao F., Lee H.-H., Farber J.M.;
 RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled receptor related to chemokine receptors and located on chromosome 6q27";
 RT Genomics 40:175-180(1997).
 RL CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC CC -1- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.
 CC CC -1- INDUCTION: BY INTERLEUKIN-2.
 CC CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.
 CC CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC CC EMBL; U45984; AAB62714.1; -;
 DR EMBL; Z79784; CAB02144.1; ALT_INIT.
 DR EMBL; U60000; AAB06949.1; -;
 DR EMBL; U68030; AAC51124.1; -;
 DR EMBL; U68032; AAC51125.1; -;
 DR HSSP; P34966; 1DDO.
 DR Genew; HGNC:1607; CCR6.
 DR MIM; 601835; -;
 DR Interpro; IPR000020; Anaphylatoxin.
 DR Interpro; IPR004067; CC_Chemine6.
 DR Interpro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR SMART; SM00104; ANATO. 1.
 DR PROSITE; PS00237; G-PROTEIN_RECEPTOR_FL1; 1.
 DR PROSITE; PS50262; G-PROTEIN_RECEPTOR_FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 47
 FT TRANSSEM 48 74
 FT DOMAIN 75 83
 FT TRANSSEM 84 104
 FT DOMAIN 105 119
 FT TRANSSEM 120 141
 FT DOMAIN 142 159
 FT TRANSSEM 160 180
 FT DOMAIN 181 211
 FT TRANSSEM 212 238
 FT DOMAIN 239 254
 FT TRANSSEM 255 279
 FT DOMAIN 280 303
 FT TRANSSEM 304 321
 FT DOMAIN 322 374
 FT DISULFID 118 197
 FT CARBOHYD 23 23
 FT CONFLICT 60 60
 FT CONFLICT 74 74
 FT CONFLICT 86 86
 FT CONFLICT 164 164
 FT CONFLICT 182 182
 FT CONFLICT 192 192
 FT CONFLICT 206 206
 E -> V (IN REF. 4).
 G -> A (IN REF. 4).
 Y -> N (IN REF. 4).
 L -> V (IN REF. 4).
 S -> T (IN REF. 5).
 T -> S (IN REF. 4).
 Q -> L (IN REF. 4).
 E -> V (IN REF. 4).

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2003, 07:12:35 ; Search time 80 Seconds
(without alignments)
880.851 Million cell updates/sec

Title: US-09-940-063-2

Perfect score: 1794

Sequence: 1 MAEHYHEDYGFSSFNDSQ.....DNKTFSSHVEATSMFOL 342

Scoring table:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Archived: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

```

1: SPREMBL_21:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1790	99.8	342	4	O9HCA5
2	1785	99.5	342	6	O9TVI6
3	1692.5	94.3	343	6	O9N0D0
4	1690.5	94.2	343	6	O9BD56
5	1332	74.2	351	11	O9EQI6
6	1326	73.9	351	11	O9ERH5
7	783	43.6	150	6	O8WNN8
8	771	43.0	149	6	O8WNN7
9	612	34.1	369	4	O9UQ06
10	605.5	33.8	367	11	O9RIV0
11	584	32.6	368	13	O42444
12	554.5	30.9	350	11	O924I3
13	551.5	30.7	350	11	O8OZM9
14	530.5	29.6	355	6	O9MT08
15	529.5	29.5	347	6	O9MZN4
16	528	29.4	346	6	O9MZN4

17	528	29.4	346	-6	O9MZN3	O9mzn3 nycticebus
18	528	29.4	346	6	O9MZN2	O9mzn2 nycticebus
19	525.5	29.3	347	6	O9MZN0	O9mzn0 alogatta se
20	525.5	29.3	347	6	O9MZN6	O9mzn6 callicebus
21	525.5	29.3	353	13	O8QPR5	O8qit5 xenopus lae
22	524.5	29.2	347	6	O9MZN9	O9mzn9 ateles pani
23	523.5	29.2	347	6	O9MZN6	O9mzn6 hylobates c
24	523.5	29.2	347	6	O9MZN5	O9mzn5 hylobates h
25	523.5	29.2	347	6	O9MZN3	O9mzn3 hylobates s
26	523.5	29.2	347	6	O9MZN2	O9mzn2 pongo pygma
27	523.5	29.2	347	6	O9MZN1	O9mzn1 gorilla gor
28	522.5	29.1	352	4	O9MZN5	O9mzn5 pithecia pi
29	522.5	29.1	347	6	O9BXA0	O9bx0 homo sapien
30	521.5	29.1	347	6	O9MZE7	O9mze7 presbytis s
31	521.5	29.1	347	6	O9MZE8	O9mze8 callithrix
32	518.5	28.9	347	6	O9MZE7	O9mze7 callimico g
33	517.5	28.8	349	11	O8VDA7	O8vda7 ratius norv
34	516.5	28.8	347	6	O9MZE6	O9mze6 presbytis j
35	516.5	28.8	347	6	O9MZE2	O9mze2 mandrillus
36	516.5	28.8	347	6	O9MZE1	O9mze1 eulemur mac
37	516	28.8	334	6	O9N1P3	O9n1p3 hylobates l
38	515.5	28.7	347	6	O9MZO3	O9mzo3 pygathrix a
39	515.5	28.7	347	6	O9MZO2	O9mzo2 rhinopithec
40	515.5	28.7	347	6	O9MZO1	O9mzo1 pygathrix b
41	515.5	28.7	347	6	O9MZO0	O9mzo0 pygathrix n
42	515.5	28.7	347	6	O9MZE9	O9mze9 nasalis lar
43	515.5	28.7	347	6	O9MZE8	O9mze8 colobus pol
44	515.5	28.7	347	6	O9MZE5	O9mze5 presbytis p
45	515.5	28.7	347	6	O9MZE4	O9mze4 presbytis f

ALIGNMENTS

RESULT 1	O9HCA5	PRELIMINARY;	PRT;	342 AA.
ID	O9HCA5			
AC	O9HCA5			
DT	01-MAR-2001 (TREMBLER, 16, Created)			
DT	01-MAR-2001 (TREMBLER, 16, Last sequence update)			
DT	01-JUN-2002 (TREMBLER, 21, Last annotation update)			
DE	Mutant G protein-coupled receptor STRL33.			
GN	STRL33.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97311099; PubMed=9166430;			
RA	Liao F., Alkhatib G., Peden K.W., Sharma G., Berger E.A., Farber J.M.;			
RT	"STRL33, A novel chemokine receptor-like protein, functions as a			
RT	fusion cofactor for both macrophage-tropic and T cell line-tropic HIV-			
RT	1."			
RL	J. Exp. Med. 185:2015-2023(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	An P., Winkler C., O'Brien S.J.;			
RT	"The Influence of a STRL33 mutant on the course of HIV-1 infection."			
RL	Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF029759; AAG21918.1;			
DR	InterPro: IPR000276; GPCR_Rhodopsn.			
DR	Pfam: PF00001; 7tm.1; 1.			
DR	PRINTS; PR00237; GPCRHHODPSN.			
DR	PRINTS; PR01568; LYMPHOTACTNR.			
DR	PROSITE; PS00237; G_PROTEIN_RECCEP_FL_1; UNKNOWN_1.			
DR	PROSITE; PS50262; G_PROTEIN_RECCEP_FL_2; 1.			
KW	Receptor.			
SO	SEQUENCE 342 AA; 39279 MW; CE149633D01D20AA CRC64;			
Query Match	99.8%; Score 1790; DB 4; Length 342;			
Best Local Similarity	99.7%; Pred. No. 4.9e-141;			
Matches 341; Conservative 1; Mismatches 0; Indels 0; Gaps 0;				

```

QY 1 MAEHDIHEDYGFSSFNDSQOEHOEFLQFSKVPFLPCMYLVVFCGLVNSLVLVISIFTH 60
D 1 MAKHDYHEDYGFSSFNDSQOEHOEFLQFSKVPFLPCMYLVVFCGLVNSLVLVISIFTH 60
QY 61 KLOSITDFVFLVNLPLADLVFVCTLPFWAYAGIHEWVGQWCKSLGITYINFTSMIL 120
D 61 KLOSITDFVFLVNLPLADLVFVCTLPFWAYAGIHEWVGQWCKSLGITYINFTSMIL 120
QY 121 TCTITVDFEIVVAKATKAYNOQAKRMWGKYSLLIWIYISLVSPQIITIGNVFNELDKLIC 180
D 121 TCTITVDFEIVVAKATKAYNOQAKRMWGKYSLLIWIYISLVSPQIITIGNVFNELDKLIC 180
QY 181 GYHDEAISTVVLATQMTLGFLLPLLMIVICYSVIITKLLHAGGFQKHSKIIIFLVMAVF 240
D 181 GYHDEAISTVVLATQMTLGFLLPLLMIVICYSVIITKLLHAGGFQKHSKIIIFLVMAVF 240
QY 241 LITOMPENLMKFIKIRSTHWEYAMTSFHYITMVEALVLRACLNPVLYAVSLKFRKNF 300
D 241 LITOMPENLMKFIKIRSTHWEYAMTSFHYITMVEALVLRACLNPVLYAVSLKFRKNF 300
QY 301 KLVKDIGCLPYLGVSQWCKSEDNSKTFSSASHNEATSMFOL 342
D 301 KLVKDIGCLPYLGVSQWCKSEDNSKTFSSASHNEATSMFOL 342

```

RESULT 2

```

QY 09TV16 PRELIMINARY; PRT; 342 AA.
AC 09TV16;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE G protein-coupled receptor STRL33.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=STRL33(BONZO);
RA Brussel A., Pretet J.L., Girard M., Butor C.;
RT "Sequences and Predicted Structures of Chimpanzee STRL33 (Bonzo) and
RT gpr15 (Bob).";
RL AIDS Res. Hum. Retroviruses 15:0-0(1999).
DR EMBL; AF084229; AAD52041.1;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PR01568; LYMPHOTACTNR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 342 AA; 39273 MW; 5B58003797806B2A CRC64;

```

Query Match 99.5%; Score 1785; DB 6; Length 342;
 Best Local Similarity 99.4%; Pred. No. 1.3e-140;
 Matches 340; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MAEHDIHEDYGFSSFNDSQOEHOEFLQFSKVPFLPCMYLVVFCGLVNSLVLVISIFTH 60
D 1 MAEHDIHEDYGFSSFNDSQOEHOEFLQFSKVPFLPCMYLVVFCGLVNSLVLVISIFTH 60
QY 61 KLOSITDFVFLVNLPLADLVFVCTLPFWAYAGIHEWVGQWCKSLGITYINFTSMIL 120
D 61 KLOSITDFVFLVNLPLADLVFVCTLPFWAYAGIHEWVGQWCKSLGITYINFTSMIL 120
QY 121 TCTITVDFEIVVAKATKAYNOQAKRMWGKYSLLIWIYISLVSPQIITIGNVFNELDKLIC 180
D 121 TCTITVDFEIVVAKATKAYNOQAKRMWGKYSLLIWIYISLVSPQIITIGNVFNELDKLIC 180
QY 181 GYHDEAISTVVLATQMTLGFLLPLLMIVICYSVIITKLLHAGGFQKHSKIIIFLVMAVF 240
D 181 GYHDEAISTVVLATQMTLGFLLPLLMIVICYSVIITKLLHAGGFQKHSKIIIFLVMAVF 240

```

```

D 181 GYHDEAISTVVLATQMTLGFLLPLLMIVICYSVIITKLLHAGGFQKHSKIIIFLVMAVF 240
QY 241 LITOMPENLMKFIKIRSTHWEYAMTSFHYITMVEALVLRACLNPVLYAVSLKFRKNF 300
D 241 LITOMPENLMKFIKIRSTHWEYAMTSFHYITMVEALVLRACLNPVLYAVSLKFRKNF 300
QY 301 KLVKDIGCLPYLGVSQWCKSEDNSKTFSSASHNEATSMFOL 342
D 301 KLVKDIGCLPYLGVSQWCKSEDNSKTFSSASHNEATSMFOL 342

```

RESULT 3

```

QY 09N020 PRELIMINARY; PRT; 343 AA.
AC 09N020;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE STRL33.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Cercopithecoidea; Cercopithecidae;
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20261727; PubMed=10799581;
RA Pohlmann S., Lee B., Meister S., Krumbiegel M., Leslie G., Doms R.W.,
RA Kirchhoff F.;
RT "Simian immunodeficiency virus utilizes human and sooty mangabey but
RT not rhesus macaque STRL33 for efficient entry.";
RL J. Virol. 74:5075-5082(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Pohlmann S., Lee B., Meister S., Krumbiegel M., Leslie G., Doms R.W.,
RA Kirchhoff F.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF237559; AAF68392.1;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PR01568; LYMPHOTACTNR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 343 AA; 39589 MW; A75B7A0751C13455 CRC64;

```

Query Match 94.3%; Score 1692.5; DB 6; Length 343;
 Best Local Similarity 94.5%; Pred. No. 6.2e-133;
 Matches 324; Conservative 9; Mismatches 9; Indels 1; Gaps 1;

```

QY 1 MAEHDIHEDYGFSSFNDSQOEHOEFLQFSKVPFLPCMYLVVFCGLVNSLVLVISIFTH 59
D 1 MAEHDIHEDYGFSSFNDSQOEHOEFLQFSKVPFLPCMYLVVFCGLVNSLVLVISIFTH 60
QY 60 HKLOSITDFVFLVNLPLADLVFVCTLPFWAYAGIHEWVGQWCKSLGITYINFTSMIL 119
D 60 HKLOSITDFVFLVNLPLADLVFVCTLPFWAYAGIHEWVGQWCKSLGITYINFTSMIL 120
QY 120 LFCITVDFEIVVAKATKAYNOQAKRMWGKYSLLIWIYISLVSPQIITIGNVFNELDKLIC 179
D 120 LFCITVDFEIVVAKATKAYNOQAKRMWGKYSLLIWIYISLVSPQIITIGNVFNELDKLIC 180
QY 180 GYHDEAISTVVLATQMTLGFLLPLLMIVICYSVIITKLLHAGGFQKHSKIIIFLVMAVF 239
D 180 GYHDEAISTVVLATQMTLGFLLPLLMIVICYSVIITKLLHAGGFQKHSKIIIFLVMAVF 240
QY 240 FLITOMPENLMKFIKIRSTHWEYAMTSFHYITMVEALVLRACLNPVLYAVSLKFRKNF 299
D 240 FLITOMPENLMKFIKIRSTHWEYAMTSFHYITMVEALVLRACLNPVLYAVSLKFRKNF 300
QY 300 KLVKDIGCLPYLGVSQWCKSEDNSKTFSSASHNEATSMFOL 342
D 300 KLVKDIGCLPYLGVSQWCKSEDNSKTFSSASHNEATSMFOL 343

```


RESULT 4

O9BDS6 PRELIMINARY: PRT: 343 AA.
 ID O9BDS6
 AC O9BDS6: (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 21, Last annotation update)
 DE Orphan seven transmembrane receptor STRL33.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 NCBI_TaxID=9541;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21134736; PubMed-11242524;
 Wade-Evans A.M., Russell J., Jenkins A., Javan C.;
 "Cloning and sequencing of cynomolgus macaque ccr3, gp15, and str133:
 potential coreceptors for HIV type 1, HIV type 2, and STV.";
 AIDS Res. Hum. Retroviruses 17:371-375(2001).
 RL EMBL, AF291671; AAK25742.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHDOPSN.
 DR PRINTS: PRO1568; LYMPHOTACNR.
 DR PROSITE: PS00237; G_PROTEIN_RECPE_FL_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECPE_FL_2; 1.
 KW Receptor; Transmembrane.
 SO SEQUENCE 343 AA; 39472 MW; 0961328F948E7784 CRC64;

Query Match 94.2%; Score 1690.5; DB 6; Length 343;
 Best Local Similarity 94.2%; Pred. No. 9.1e-133;
 Matches 323; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

QY 1 MAEDYHEDYGF--SSFNDSOEHQDFLQFSKVEFLPCMYLVVFCGLVNSLVVISIFY 59
 1 MAEDYHEDYGF--SSFNDSOEHQDFLQFSKVEFLPCMYLVVFCGLVNSLVVISIFY 59
 DB 1 MAEDYHEDYGF--SSFNDSOEHQDFLQFSKVEFLPCMYLVVFCGLVNSLVVISIFY 60
 QY 60 HKLOSLDVLVNLPLADLVVCTLPFWAVAGIHEWVFGVWCKSLGITYINITYSMLI 119
 61 HKLOSLDVLVNLPLADLVVCTLPFWAVAGIHEWVFGVWCKSLGITYINITYSMLI 120
 DB 61 HKLOSLDVLVNLPLADLVVCTLPFWAVAGIHEWVFGVWCKSLGITYINITYSMLI 120
 QY 120 LTCITVDFEIVVATKATAYNOAKRMWGKVTSLIWIYSLVSLPDIYGNVNDKLI 179
 121 LTCITVDFEIVVATKATAYNOAKRMWGKVTSLIWIYSLVSLPDIYGNVNDKLI 180
 DB 121 LTCITVDFEIVVATKATAYNOAKRMWGKVTSLIWIYSLVSLPDIYGNVNDKLI 180
 QY 180 CGYHDEAISTVVLATQMTLGFPLTLIMVICYSVIIRTLHAGGFQKRSKIIFLVAV 239
 181 CGYHDEAISTVVLATQMTLGFPLTLIMVICYSVIIRTLHAGGFQKRSKIIFLVAV 240
 DB 181 CGYHDEAISTVVLATQMTLGFPLTLIMVICYSVIIRTLHAGGFQKRSKIIFLVAV 240
 QY 240 FLTLQMPFNLMKFRSTHMEYVAMTSFRHYTMTVEALAYLACINPVLAYAVSLKFRNF 299
 241 FLTLQMPFNLMKFRSTHMEYVAMTSFRHYTMTVEALAYLACINPVLAYAVSLKFRNF 300
 DB 241 FLTLQMPFNLMKFRSTHMEYVAMTSFRHYTMTVEALAYLACINPVLAYAVSLKFRNF 300
 QY 300 WKLVKDIGCLPYLGVSHQWKSSEDSKTFSSASHNVATSMFQL 342
 301 WKLVKDIGCLPYLGVSHQWKSSEDSKTFSSASHNVATSMFQL 343
 DB 301 WKLVKDIGCLPYLGVSHQWKSSEDSKTFSSASHNVATSMFQL 343

RESULT 5

O9E016 PRELIMINARY: PRT: 351 AA.
 ID O9E016
 AC O9E016: (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Chemokine receptor CXCR6.
 GN CXCR6.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.
 RN STRAIN=C57BL/6;
 RC MEDLINE-21177382; PubMed-11017100;
 RA MacLoudian M., David A., Engel S., Ryan J.E., Cyster J.G.;
 "A transmembrane CXC chemokine is a ligand for HIV-coreceptor Bonzo."
 Nat. Immunol. 1:298-304(2000).
 RL EMBL, AF301018; AAC34367.1; -
 DR MGD; MGI:1934582; Cxcr6.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHDOPSN.
 DR PRINTS: PRO1568; LYMPHOTACNR.
 DR PROSITE: PS00237; G_PROTEIN_RECPE_FL_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECPE_FL_2; 1.
 KW Receptor.
 SO SEQUENCE 351 AA; 40468 MW; 5658788372B4C65A CRC64;

Query Match 74.2%; Score 1332; DB 11; Length 351;
 Best Local Similarity 75.2%; Pred. No. 5.8e-103;
 Matches 258; Conservative 36; Mismatches 47; Indels 2; Gaps 1;

QY 2 AEHDYHEDYGFSSFNDS--QEHQDFLQFSKVEFLPCMYLVVFCGLVNSLVVISIFY 59
 2 AEHDYHEDYGFSSFNDS--QEHQDFLQFSKVEFLPCMYLVVFCGLVNSLVVISIFY 59
 DB 9 ALYDGYEGDEWFLNNSSDNSQENKRFLEKVEFLPCYLVVFCGLVNSLVVISIFY 68
 QY 60 HKLOSLDVLVNLPLADLVVCTLPFWAVAGIHEWVFGVWCKSLGITYINITYSMLI 119
 61 HKLOSLDVLVNLPLADLVVCTLPFWAVAGIHEWVFGVWCKSLGITYINITYSMLI 120
 DB 61 HKLOSLDVLVNLPLADLVVCTLPFWAVAGIHEWVFGVWCKSLGITYINITYSMLI 120
 QY 120 LTCITVDFEIVVATKATAYNOAKRMWGKVTSLIWIYSLVSLPDIYGNVNDKLI 179
 121 LTCITVDFEIVVATKATAYNOAKRMWGKVTSLIWIYSLVSLPDIYGNVNDKLI 180
 DB 121 LTCITVDFEIVVATKATAYNOAKRMWGKVTSLIWIYSLVSLPDIYGNVNDKLI 180
 QY 180 CGYHDEAISTVVLATQMTLGFPLTLIMVICYSVIIRTLHAGGFQKRSKIIFLVAV 239
 181 CGYHDEAISTVVLATQMTLGFPLTLIMVICYSVIIRTLHAGGFQKRSKIIFLVAV 240
 DB 181 CGYHDEAISTVVLATQMTLGFPLTLIMVICYSVIIRTLHAGGFQKRSKIIFLVAV 240
 QY 240 FLTLQMPFNLMKFRSTHMEYVAMTSFRHYTMTVEALAYLACINPVLAYAVSLKFRNF 299
 241 FLTLQMPFNLMKFRSTHMEYVAMTSFRHYTMTVEALAYLACINPVLAYAVSLKFRNF 300
 DB 241 FLTLQMPFNLMKFRSTHMEYVAMTSFRHYTMTVEALAYLACINPVLAYAVSLKFRNF 300
 QY 300 WKLVKDIGCLPYLGVSHQWKSSEDSKTFSSASHNVATSMFQL 342
 301 WKLVKDIGCLPYLGVSHQWKSSEDSKTFSSASHNVATSMFQL 351
 DB 301 WKLVKDIGCLPYLGVSHQWKSSEDSKTFSSASHNVATSMFQL 351

RESULT 6

O9ERH5 PRELIMINARY: PRT: 351 AA.
 ID O9ERH5
 AC O9ERH5: (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Putative chemokine receptor.
 GN CXCR6.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=SPLEEN;
 RA Sato H., Taniguchi M.;
 "Molecular cloning of a putative chemokine receptor preferentially
 expressed in mouse lymphocytes."
 submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL, AF305709; AAC31284.1; -
 DR MGD; MGI:1934582; Cxcr6.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHDOPSN.

```

DR PRINTS: PRO1568; LYMPHOTACTNR.
DR PROSITE: PS00337; G_PROTEIN_RECIP_FL_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECIP_FL_2; 1.
KW Receptor.
SQ SEQUENCE      351 AA; 40511 MW; B00E3134D2B4DIED CRC64;

Query Match          73.9%; Score 1326; DB 11; Length 351;
Best Local Similarity 74.9%; Pred. No. 1.8e-102;
Matches 257; Conservative 36; Mismatches 48; Indels 2; Gaps 1.

OY 2 AEHDYHEDYGRSSFNDS--OEHEODFLQFSKVFLEPCMYLVFVCGLVGNSLVIYSIFY 59
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 9 ALYGHGYEGDEWLFENNDSDNNOENRFLFKFEVEFLPCYILVLYFVGGLGNLSVLITIFY 68
   |||:|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 60 HKLOSIDVFLVNLPLADLVFCVLPFAVAAGIHFWFGYOVCCKSLGIYIINFYTMLI 119
   |||:|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 69 QKRLFDIVFLNPLADLVFECVLPFAVAAGTYEWGVGTVMCKTLRGMTYMNFYVSMLT 128
   |||:|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 120 LFTCTVDDEFIVVATKAYNQOAKRMFGKXTSLIIWIISLLVSLPQITYGAVNFLDKLI 179
   |||:|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 129 LTCITVDDEFIVVQATKAFNNQAKRMIGOVICLIIWVASLVLSLPQITIGHVODIKLI 188
   |||:|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 180 CGYHDEAISTVVALTQMILGFELPLMTIYCVSVITIKTLFHAGGFOKRSRKLIFFLVAV 239
   |||:|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 189 CQYHSEELSTMVLYQMRGFFFLPLTIMILCYSGIKTLFLARNRQKRKSLLKIIFLVAV 248
   |||:|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 240 FLLTPMPENLMKFIIRSTHWEEYYAMTSFYHTIMVTETALVYLACLNPLYLAFVSLEFRNF 299
   |||:|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 249 FLITOTPENLMLLIOSTSWEMYYITTSFKYAIVVTEAIYFPACINPLYLAFAVGLEFRKNV 308
   |||:|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 300 WKIWKDIGCLPYLGVSHOWKSSSPSKSFSSAHNEAFMSRL 342
   |||:|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 309 WKLMDIGCLSHLGVSQMKSSSDSKTCSASHNETISMFL 351
   |||:|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
O8WNMB PRELIMITARY: PRT: 150 AA.
AC O8WNMB:
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Chemokine receptor 2 (Fragment).
CN CCR2.
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Gorilla.
OX NCBI_TaxId=9593;
RN [1]
FR SEQUENCE FROM N.A.
FR Stauffer R.L., Walker A., Ryder O., Lyons-Weller M., Hedges S.B.;
FR "Human and ape molecular clocks and constraints on paleontological
FR hypotheses.";
RL J. Hered. 92:0-0(2001).
DB EMBL, AF354630; AAL56234.1; -
DB InterPro: IPR00276; GPCR_Rhodopsn.
DB Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_HODOPSN.
DR PROSITE: PS50262; G_PROTEIN_RECIP_FL_2; 1.
KW Receptor.
FT NON_TER      1
FT NON_TER      1
SQ SEQUENCE     150 AA; 17352 MW; C5427C09AB0502EB CRC64;

Query Match          43.6%; Score 783; DB 6; Length 150;
Best Local Similarity 99.3%; Pred. No. 1.1e-57;
Matches 149; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 172 VFNDKILCGYHDAISTVVALTQMILGFELPLMTIYCVSVITIKTLFHAGGFQKRHSK 231
   |||:|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 VFNDKILCGYHDAISTVVALTQMILGFELPLMTIYCVSVITIKTLFHAGGFQKRHSK 60
   |||:|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 232 TFFLVMAVFLLTPMPENLMKFIIRSTHWEEYYAMTSFYHTIMVTETALVYLACLNPLYLA 291

```

DB	61	ITFLVAVPELLTQMPFNLMKLRSHMEYAMTSHYTIMTEAIALIRACLNPVLAFAV	120
QY	292	SLKFRKFMKLVKIDICLPYLGVSHQWMS	321
Db	121	SLKFRKFMKLVKIDICLPYLGVSHQWMS	150
RESULT 8			
Q8WMN7	PRELIMINARY;	PRT;	149 AA.
Q8WMN7			
AC	08WMN7		
DT	01-MAR-2002 (TReMBLrel. 20, Created)		
DT	01-MAR-2002 (TReMBLrel. 20, Last sequence update)		
DT	01-JUN-2002 (TReMBLrel. 21, Last annotation update)		
De	Chemokine receptor 2 (Fragment).		
GN	CCR2.		
OS	Pongo pygmaeus (Orangutan).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.		
OX	NCBI_TaxID=9600;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Stauffer R.L., Walker A., Ryder O., Lyons-Weiler M., Hedges S.B.;		
RT	"Human and ape molecular clocks and constraints on paleontological		
RT	hypotheses."		
RL	J. Hered. 92:0-0(2001).		
DR	EMBL; AF354631; AAL56235.1;		
DR	InterPro; IPR000276; GPCR_Rhodopsn.		
DR	Pfam; PF00001; 7tm.1; 1.		
DR	PRINTS; PR00237; GPCR_RHODOPS.		
DR	PROSITE; P550262; G_PROTEIN_RECEP_F1_2; 1.		
KW	Receptor.		
FT	NON_TER	1	
FT	NON_TER	149	
SQ	SEQUENCE	149 AA; 17256 MW; DB8FD8461356CF85 CRC64;	
Query Match 43.0%; Score 771; DB 6; Length 149;			
Best Local Similarity 98.7%; Pzed. No. 1e-56;			
Matches 147; Conservative 0; Mismatches 2; Indels 0; Gaps 0			
QY	172	VENLDDLTGIGHDEAISTVYLATQMTLGFPLPLTMTVCSVITKTLHHGSGQKRRSLK	231
Db	1	VENLDDLTGIGHDEAISTVYLATQMTLGFPLPLTMTVCSVITKTLHGGGQKRRSLK	60
QY	232	IIFLVAVEPLTQMPFNLMKRFIRSTHMEYAMTSEHYTIMTEAIALIRACLNPVLAFAV	291
Db	61	IIFLVAVEPLTQMPFNLMKLRSHMEYAMTSHYTIMTEAIALIRACLNPVLAFAV	120
QY	292	SLKFRKFMKLVKIDICLPYLGVSHQWMS	320
Db	121	SLKFRKFMKLVKIDICLPYLGVSHQWMS	149
RESULT 9			
Q9UQ06	PRELIMINARY;	PRT;	369 AA.
Q9UQ06			
AC	Q9UQ06		
DT	01-MAY-2000 (TReMBLrel. 13, Created)		
DT	01-MAY-2000 (TReMBLrel. 13, Last sequence update)		
DT	01-JUN-2002 (TReMBLrel. 21, Last annotation update)		
De	Chemokine receptor CCR9 (CC chemokine receptor 9A).		
GN	CCR9.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE=99248139; PubMed=10229797;		
RX	Zaballos A., Gutierrez J., Varona R., Ardayin C., Marquez G.;		
RT	"Identification of the orphan chemokine receptor GPR-9-6 as CCR9, the		
RT	receptor for the chemokine TECK."		

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2003, 07:01:55 ; Search time 72 Seconds
(without alignments)
632.940 Million cell updates/sec

Title: US-09-940-063-2
Perfect score: 1794
Sequence: 1 MAEDHEDYGFSSFNDSQ.....DNKTFSSHNEATSMFQL 342

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Archived: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1:	/SIDSeq_101002.*
2:	/SIDSeq/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
3:	/SIDSeq/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
4:	/SIDSeq/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
5:	/SIDSeq/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
6:	/SIDSeq/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
7:	/SIDSeq/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
8:	/SIDSeq/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
9:	/SIDSeq/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
10:	/SIDSeq/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
11:	/SIDSeq/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
12:	/SIDSeq/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
13:	/SIDSeq/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
14:	/SIDSeq/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
15:	/SIDSeq/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
16:	/SIDSeq/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
17:	/SIDSeq/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
18:	/SIDSeq/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
19:	/SIDSeq/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
20:	/SIDSeq/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
21:	/SIDSeq/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SIDSeq/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SIDSeq/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1794	100.0	342	19	AAW80806
2	1794	100.0	342	19	AAW80806
3	1794	100.0	342	20	AAW80806
4	1794	100.0	342	20	AAW80806
5	1794	100.0	342	22	AAW80806
6	1794	100.0	342	22	AAW80806
7	1794	100.0	342	22	AAW80806
8	1794	100.0	342	22	AAW80806
9	1794	100.0	342	22	AAW80806
10	1730	96.4	342	20	AAW80806

11	1730	96.4	342	22	AAU04034
12	1717	95.7	342	20	AAW97784
13	1717	95.7	342	22	AAU04033
14	1332	74.2	351	20	AAW23825
15	1049	58.5	302	19	AAW70001
16	619	34.5	369	22	AAW80113
17	619	34.5	374	22	AAW80112
18	619	34.5	374	22	AAW80112
19	612	34.1	357	21	AAW90605
20	612	34.1	357	21	AAW90605
21	612	34.1	357	22	AAW80117
22	612	34.1	357	22	AAW80116
23	608.5	33.9	358	15	AAW83745
24	608.5	33.9	358	21	AAW81689
25	608.5	33.9	358	23	AAW91231
26	608.5	33.9	378	15	AAW83744
27	608.5	33.9	378	19	AAW8774
28	608.5	33.9	378	21	AAW81688
29	608.5	33.9	378	21	AAW81689
30	608.5	33.9	378	21	AAW90629
31	608.5	33.9	378	22	AAW80114
32	608.5	33.9	378	22	AAW80859
33	608.5	33.9	378	23	AAW91230
34	608.5	33.9	410	15	AAW91241
35	608.5	33.9	410	19	AAW8723
36	608.5	33.9	410	21	AAW81687
37	608.5	33.9	410	21	AAW81687
38	608.5	33.9	410	23	AAW91229
39	608.5	33.9	569	22	AAW90649
40	606	33.8	357	21	AAW90649
41	606	33.8	359	15	AAW83747
42	606	33.8	359	19	AAW8728
43	606	33.8	359	21	AAW81691
44	606	33.8	359	23	AAW91233
45	606	33.8	369	22	AAW56344

ALIGNMENTS

RESULT 1	AAW80806	AAW80806 standard; Protein: 342 AA.	
XX	AAW80806;		
XX	22-JAN-1999 (first entry)		
DT	STRL33 protein sequence.		
DE	STRL33; human; HIV-1; HIV related disorder; therapy; CD4; diagnosis;		
XX	fusion accessory factor.		
KW	Homo sapiens.		
XX	MO9844098-A2.		
PN	08-OCT-1998.		
PD	31-MAR-1998; 98WO-US06517.		
XX	31-MAR-1997; 97US-0042880.		
XX	(USSH) US SEC HEALTH & HUMAN SERVICES.		
PA	Alkhalib G, Berger EA, Farber JM, Liao F;		
XX	WPI; 1998-557107/47.		
XX	N-PSDB; AAW8515.		
DR	New isolated fusion accessory factor STRL33 - which mediates HIV		
XX	infection of cells, used to develop products for the study,		
PT	prevention and therapy of HIV-related disorders		
PT			

XX Claim 65; Fig 4; 74pp; English.

XX
XX This sequence is the human STRL33 polypeptide that is expressed by
CC the recombinant cell line of the invention. The STRL33 polypeptide is a
CC fusion accessory factor that can function with CD4 to mediate fusion with
CC cells bearing HIV-1 env from both laboratory-adapted TCR-tropic variants
CC and from M-tropic variants. Agents that suppress STRL33 can be used in a
CC method to treat HIV-related disorders. The products and methods can be
CC used for the study, prevention and therapy of HIV-related disorders.

XX
XX Sequence 342 AA:

Query Match 100.0%; Score 1794; DB 19; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.4e-180; Indels 0; Gaps 0;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEHDYHEDYGFSSFNDSOEHDQDFQSKVFLPCMTLVFVCGVGNLSLVYISIFYH 60
DB 1 MAEHDYHEDYGFSSFNDSOEHDQDFQSKVFLPCMTLVFVCGVGNLSLVYISIFYH 60
DB 61 KLSQSLDFVFLVNLPLADLVFVCTLPFMAVAGIHEWFGQVCKSLGITYTINFTSMIL 120
DB 61 KLSQSLDFVFLVNLPLADLVFVCTLPFMAVAGIHEWFGQVCKSLGITYTINFTSMIL 120
DB 61 KLSQSLDFVFLVNLPLADLVFVCTLPFMAVAGIHEWFGQVCKSLGITYTINFTSMIL 120
QY 121 TCITVDFRIVVVKATKAKAQQAKRMWCKVTSLLIWIISLVSLPQITTYGVNFDKILC 180
DB 121 TCITVDFRIVVVKATKAKAQQAKRMWCKVTSLLIWIISLVSLPQITTYGVNFDKILC 180
QY 181 GYHDEAISTVVLATQMTLGFPLPLTMIVCYSVITKLLHAGGQKRSKIIIFLVMAVF 240
DB 181 GYHDEAISTVVLATQMTLGFPLPLTMIVCYSVITKLLHAGGQKRSKIIIFLVMAVF 240
QY 241 LLTQMPENLMKFIRSTHMEYYAMTSFHYTIVTEAIAVLRACLNPVLYAFVSLFRKNFW 300
DB 241 LLTQMPENLMKFIRSTHMEYYAMTSFHYTIVTEAIAVLRACLNPVLYAFVSLFRKNFW 300
QY 301 KLVKDIGCLPYLGVSQWKSSEDNSKTFPSASHNVEATSMFOL 342
DB 301 KLVKDIGCLPYLGVSQWKSSEDNSKTFPSASHNVEATSMFOL 342

RESULT 2
ID AAM54041
AA AAM54041 standard; Protein: 342 AA.
XX
AC AAM54041;
XX
DT 07-AUG-1998 (first entry)
XX
XX Human HBMBU14 protein.
XX
KW Human; 7-transmembrane receptor; HBMBU14; infection; HIV; cancer; asthma;
KW anorexia; Parkinson's disease; acute heart failure; atherosclerosis;
KW osteoporosis; angina pectoris; myocardial infarction; psychotic disorder;
KW benign prostatic hypertrophy; neurological disorder; therapy;
KW Huntington's disease; Gilles de la Tourette's syndrome.
XX
OS Homo sapiens.
XX
XX EP834563-A2.
XX
XX PD 08-APR-1998.
XX
XX PF 23-SEP-1997; 97EP-0307428.
XX
XX PR 26-SEP-1996; 96US-0026669.
XX
XX PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
XX FI Bergsma DJ, Ellis CE, Elshourbagy NA;
XX
XX WPI; 1998-208924/19.

DR N-PSDB; AAV24017.
XX
XX
XX New isolated human 7-trans-membrane receptor, HBMBU14 - useful for
PT developing products for treating, e.g. infections, pain, cancers,
PT anorexia, hypotension, osteoporosis and asthma
XX
XX Claim 12; Fig 1; 36pp; English.

XX
XX This sequence is the human HBMBU14 protein of the invention. HBMBU14
CC is a human 7-transmembrane (TM) receptor. The products can be used for
CC treating or preventing conditions related to abnormal HBMBU14 expression
CC or activity, e.g. infections such as bacterial, fungal, protozoan and
CC viral infections especially infections caused by HIV-1 and HIV-2, pain,
CC cancers, anorexia, bulimia, asthma, Parkinson's disease, acute heart
CC failure, atherosclerosis, hypotension, hypertension, urinary retention,
CC osteoporosis, angina pectoris, myocardial infarction, ulcers, asthma,
CC allergies, benign prostatic hypertrophy and psychotic and neurological
CC disorders, including anxiety, schizophrenia, manic depression, delirium,
CC dementia or severe mental retardation, and dyskinesias, such as
CC Huntington's disease or Gilles de la Tourette's syndrome. The products
CC can also be used for diagnosing a disease or susceptibility to a disease
CC related to the expression of HBMBU14 and for identifying compounds which
CC bind to and activate or inhibit a receptor for the polypeptide.

XX
XX Sequence 342 AA:

Query Match 100.0%; Score 1794; DB 19; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.4e-180; Indels 0; Gaps 0;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEHDYHEDYGFSSFNDSOEHDQDFQSKVFLPCMTLVFVCGVGNLSLVYISIFYH 60
DB 1 MAEHDYHEDYGFSSFNDSOEHDQDFQSKVFLPCMTLVFVCGVGNLSLVYISIFYH 60
DB 61 KLSQSLDFVFLVNLPLADLVFVCTLPFMAVAGIHEWFGQVCKSLGITYTINFTSMIL 120
DB 61 KLSQSLDFVFLVNLPLADLVFVCTLPFMAVAGIHEWFGQVCKSLGITYTINFTSMIL 120
DB 61 KLSQSLDFVFLVNLPLADLVFVCTLPFMAVAGIHEWFGQVCKSLGITYTINFTSMIL 120
QY 121 TCITVDFRIVVVKATKAKAQQAKRMWCKVTSLLIWIISLVSLPQITTYGVNFDKILC 180
DB 121 TCITVDFRIVVVKATKAKAQQAKRMWCKVTSLLIWIISLVSLPQITTYGVNFDKILC 180
QY 181 GYHDEAISTVVLATQMTLGFPLPLTMIVCYSVITKLLHAGGQKRSKIIIFLVMAVF 240
DB 181 GYHDEAISTVVLATQMTLGFPLPLTMIVCYSVITKLLHAGGQKRSKIIIFLVMAVF 240
QY 241 LLTQMPENLMKFIRSTHMEYYAMTSFHYTIVTEAIAVLRACLNPVLYAFVSLFRKNFW 300
DB 241 LLTQMPENLMKFIRSTHMEYYAMTSFHYTIVTEAIAVLRACLNPVLYAFVSLFRKNFW 300
QY 301 KLVKDIGCLPYLGVSQWKSSEDNSKTFPSASHNVEATSMFOL 342
DB 301 KLVKDIGCLPYLGVSQWKSSEDNSKTFPSASHNVEATSMFOL 342

RESULT 3
ID AAY39366
AA AAY39366 standard; Protein: 342 AA.
XX
XX AAY39366;
XX
XX DT 05-JAN-2000 (first entry)
XX
XX DE Platelet factor-4 (PF-4) receptor amino acid sequence.
XX
XX
XX PF-4; platelet factor-4; alpha granules; collagen; thrombotic stimuli;
KW thrombosis; inflammatory activity; chemokine; PF-4 receptor; HBMBU14;
KW BONZO; TTMSTR; agonist; antagonist; HIV; AIDS; rheumatoid arthritis;
KW asthma; psoriasis; atherosclerosis; inflammatory disorder.
XX
XX OS Homo sapiens.
XX
XX PN WO9950670-A1.

PD 07-OCT-1999.
XX
XX 26-MAR-1999; 99WO-GB00950.
XX
XX 27-MAR-1998; 98GB-0006677.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Macphee CH, Moores K, Berkhout TA;
XX
XX WPI: 1999-591378/50.
DR N-PSDB; AAZ28362.
XX
XX
PT Novel PF-4 receptor assays used to identify antagonists and agonists of
PT the receptor for use in therapy -
XX
PS Example 1; Page 27-28; 35pp; English.

This sequence is the platelet factor-4 (PF-4) receptor amino acid sequence. PF-4 is a 70 residue polypeptide released from alpha-granules when platelets are activated by contacting collagen or other thrombotic stimuli. PF-4 promotes thrombosis at sites of platelet activation, and also exhibits several inflammatory activities. The carboxy terminal tripeptide of PF-4 is a potent chemotactic agent for monocytes. PF-4 is a CXCR1 chemokine. The PF-4 receptor, also known as HBHNU14, TYRSTR and BOM20, is used in the methods of the invention. The invention relates to a novel screening method for identifying antagonists and agonists of the PF-4 receptor, involving using PF-4 and the PF-4 receptor together. PF-4 and the PF-4 receptor are used to identify further chemokine ligands for the receptor using a competitive binding assay and labelled PF-4. PF-4 is used to identify neutralizing or activating antibodies to the PF-4 receptor for use in therapy. PF-4 can be used in a screening method for identifying an antagonist of the receptor. Antagonists and agonists may be used for therapeutic purposes, such as treatment of HIV, AIDS, rheumatoid arthritis, asthma, psoriasis, atherosclerosis, and other inflammatory diseases.

Sequence 342 AA;
SQ

Query Match	100.0%	Score 1794	DB 20	Length 342
Best Local Similarity	100.0%	Pred. No. 1.4e-180		
Matches 342	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MAEHDYHEDYGFSSFNDSOEHODLQFSKVELPCMYLVYFVCGLVGNSLVLVISIFYH	60	
	1	MAEHDYHEDYGFSSFNDSOEHODLQFSKVELPCMYLVYFVCGLVGNSLVLVISIFYH	60	
QY	61	KLOSITDVELNLPLADLVFCYCTLPFMAVAGIHEVFEQVWCKSLIGITTYINFTYSMLT	120	
	61	KLOSITDVELNLPLADLVFCYCTLPFMAVAGIHEVFEQVWCKSLIGITTYINFTYSMLT	120	
QY	121	TCITVDREIIVVKKATKAYNQOAKRMTWGKVTSLTIWISLVSPLQIITYGNVFNLDKLC	180	
	121	TCITVDREIIVVKKATKAYNQOAKRMTWGKVTSLTIWISLVSPLQIITYGNVFNLDKLC	180	
QY	181	GYHDEAISTVVLATQMTIGFFLPRLTMTVVCYVYIYKTLTHAGGFGKHSKLTIFLYMAVF	240	
	181	GYHDEAISTVVLATQMTIGFFLPRLTMTVVCYVYIYKTLTHAGGFGKHSKLTIFLYMAVF	240	
QY	241	LLTQMPFNLMEFIRSTHWEYFAMTSFHTINWTEAIVLRACINVLVLAFFVSLKFRKNFM	300	
	241	LLTQMPFNLMEFIRSTHWEYFAMTSFHTINWTEAIVLRACINVLVLAFFVSLKFRKNFM	300	
QY	301	KLVKDIGCLPYLGVSHQWKSSEDNSKTFSSASHNVEATSMFOL	342	
	301	KLVKDIGCLPYLGVSHQWKSSEDNSKTFSSASHNVEATSMFOL	342	
Db				

RESULT 4

AAW97783

ID AAW97783 standard; Protein: 342 AA.

AC	AAW97783;	
XX		
DT	21-MAY-1999	(first entry)
XX		
DE	Human HIV/SIV receptor protein Bonzo.	
XX		
KW	SIV receptor; HIV receptor; Bonzo; translocation promoting agent;	
KW	human; G protein coupled receptor; chemokine receptor; AIDS;	
KW	infection; virus transmission.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Misc-difference 53	
FT	/note= "encoded by TG"	
FT	Misc-difference 9..71	
FT	/note= "encoded by TG"	
FT	Misc-difference 102	
FT	/note= "encoded by CG"	
XX		
PN	WO9903868-A1.	
XX		
PD	28-JAN-1999.	
XX		
PF	17-JUL-1998;	98WO-US14857.
XX		
PR	17-JUL-1997;	97US-0896155.
XX		
XX	(UYNX) UNIV NEW YORK STATE.	
PA		
XX		
PI	Deng H, Kewalramani VN, Littman DR, Unutmaz D;	
XX		
DR	WPI: 1999-132164/11.	
XX	N-PSDB; AAX07289.	
PT	New nucleic acid encoding the human translocation promoter Bonzo -	
PT	used to screen for potential agents for treating acquired immune	
PT	deficiency syndrome	
XX		
PS	Claim 4; Page 78-79; 97pp; English.	
XX		
CC	This is the amino acid sequence of human Bonzo, a novel HIV/SIV	
CC	translocation promoting agent that acts in conjunction with CD4 to	
CC	serve as a receptor for the entry into a cell of a virus having a	
CC	specific viral envelope glycoprotein. Bonzo is a member of the	
CC	7-transmembrane G-protein coupled receptor family, is closely	
CC	related to the chemokine receptor family, and is expressed in	
CC	lymphoid tissues. The invention provides the amino acid sequences	
CC	(see AAW97783-88) and DNA sequences (see AAX07289-94) of human,	
CC	African green monkey and pig-tailed macaque Bonzo and Bob (brother	
CC	of Bonzo) translocation promoting agents. These novel receptors	
CC	were identified using an expression cloning strategy. They were	
CC	found to be used by particular strains of HIV-2 and M-tropic HIV-1.	
CC	The invention also includes: mammalian cells transfected with Bonzo	
CC	and/or Bob and human CD4, which can be used to screen potential	
CC	therapeutic agents and identify ligands; antibodies to Bonzo, which	
CC	can be used therapeutically, e.g. as antagonists or to target	
CC	toxins or radioisotopes to HIV-permissive cells; transgenic	
CC	animals; and antisense and ribozyme molecules, which may also be	
CC	used therapeutically, particularly expressed from a gene therapy	
CC	vector.	
XX		
SQ	Sequence 342 AA;	
XX		
Query Match	100.0%; Score 1794; DB 20; Length 342;	
Best Local Similarity	100.0%; Pred. No. 1,4e-180;	
Matches 342; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	

Query Match	100.0%	Score 1794	DB 20	Length 342
Best Local Similarity	100.0%	Pred. No. 1,4e-180		
Matches	342	Conservative 0	Mismatches 0	Indels 0
				Gaps 0

QY	1	MAEHDDYEDYGFSSFNDDSOEHQDFLOFSKYFLPCMYLVVCGVGNLSLVLYSTYH	60
DB	1	MAEHDDYEDYGFSSFNDDSOEHQDFLOFSKYFLPCMYLVVCGVGNLSLVLYSTYH	60
QY	61	KLQSTLDVFLNPLPADLVFVCTLLPFMYAGIIEHVEFGVCKSLLGITYTINFTYMLIL	120

|||||
Db 61 KLSQSTDFEVLNPLADLVFVCTLPFMAVAGIHEWVFGVCKSLGITYTINFTSMIL 120
QY 121 TCIYVDRFIVVKKATKAVNOQAKRTWGRKTSLSLIWISLVSLPQIITYGNVFNLDKILC 180
Db 121 TCIYVDRFIVVKKATKAVNOQAKRTWGRKTSLSLIWISLVSLPQIITYGNVFNLDKILC 180
QY 181 GYHDEAISTVVLATQMTLGFPLPLTMIVCYSVIIKTLHAGGFGQKHSKIIFFLVMAVF 240
Db 181 GYHDEAISTVVLATQMTLGFPLPLTMIVCYSVIIKTLHAGGFGQKHSKIIFFLVMAVF 240
QY 241 LITOMPENLMKFIIRSTHEEYAMTSFHTIWTETAIALRACLNPLVLAFAVSLKFRKNFW 300
Db 241 LITOMPENLMKFIIRSTHEEYAMTSFHTIWTETAIALRACLNPLVLAFAVSLKFRKNFW 300
QY 301 KLVKDIGCLPYLGVSQWKSSEDNSKTPSASHNVEATSMFOL 342
Db 301 KLVKDIGCLPYLGVSQWKSSEDNSKTPSASHNVEATSMFOL 342

RESULT 5

AA680125 standard; Protein; 342 AA.

AA680125;

17-JAN-2002 (first entry)

Human CXCR6 protein.

Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
chronic bowel inflammation; rheumatoid arthritis; cytostatic;
antihistaminic; antitubercular; immunosuppressive; dermatological;
antirheumatic; antitubercular.

Homo sapiens.

WO200172830-A2.

04-OCT-2001.

02-APR-2001; 2001WO-EP03708.

31-MAR-2000; 2000DE-1016013.

(IPFP-) IPF PHARM GMBH.

(FORS/) FORSMANN U.

Forsmann W, Adermann K, Heitland A, Spodsborg N;

WPI: 2001-626256/72.

Diagnostic agent containing two or more receptor-specific ligands,
useful for detecting tumors, inflammation etc., also therapeutic use of
ligand inhibitors

Disclosure; Page 13; 26pp; German.

This invention describes a novel diagnostic agent (A) comprising at least
two different ligands (I) for receptors (II) that are implicated in
disease. (A) are used for the diagnosis of tumors (especially colorectal
or prostatic), organ rejection, inflammation and autoimmune diseases.
Also inhibitors of (I) are used therapeutically against tumors (and their
metastases), inflammation (particularly bronchial asthma or chronic bowel
inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
endocrine, motor or urogenital systems or skin are affected, and bone
marrow diseases. The products of the invention are chemokine derivatives
which have cytostatic, antiinflammatory, antisthmatic,
immunosuppressive, dermatological, antihistaminic, antitubercular,
chemokines act on specific tumor and inflammatory cells through a
constellation of chemokine receptors (CR), which control migration and

CC proliferation of these cells. AA680045-AA680128 represent human chemokine
fragments used to illustrate the method of the invention.

CC Sequence 342 AA:

Query Match 100.0%; Score 1794; DB 22; Length 342;
Best Local Similarity 100.0%; Pred. No. 1,4e-180;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEHDYHEDYGFSSSEDSOEHODLOFSKVFPCMYLVFVCGLVGNSLVVISIFVH 60
Db 1 MAEHDYHEDYGFSSSEDSOEHODLOFSKVFPCMYLVFVCGLVGNSLVVISIFVH 60
QY 61 KLSQSTDFEVLNPLADLVFVCTLPFMAVAGIHEWVFGVCKSLGITYTINFTSMIL 120
Db 61 KLSQSTDFEVLNPLADLVFVCTLPFMAVAGIHEWVFGVCKSLGITYTINFTSMIL 120
QY 121 TCIYVDRFIVVKKATKAVNOQAKRTWGRKTSLSLIWISLVSLPQIITYGNVFNLDKILC 180
Db 121 TCIYVDRFIVVKKATKAVNOQAKRTWGRKTSLSLIWISLVSLPQIITYGNVFNLDKILC 180
QY 181 GYHDEAISTVVLATQMTLGFPLPLTMIVCYSVIIKTLHAGGFGQKHSKIIFFLVMAVF 240
Db 181 GYHDEAISTVVLATQMTLGFPLPLTMIVCYSVIIKTLHAGGFGQKHSKIIFFLVMAVF 240
QY 241 LITOMPENLMKFIIRSTHEEYAMTSFHTIWTETAIALRACLNPLVLAFAVSLKFRKNFW 300
Db 241 LITOMPENLMKFIIRSTHEEYAMTSFHTIWTETAIALRACLNPLVLAFAVSLKFRKNFW 300
QY 301 KLVKDIGCLPYLGVSQWKSSEDNSKTPSASHNVEATSMFOL 342
Db 301 KLVKDIGCLPYLGVSQWKSSEDNSKTPSASHNVEATSMFOL 342

RESULT 6

AA679091 standard; Protein; 342 AA.

AA679091;

10-DEC-2001 (first entry)

Amino acid sequence of a human polypeptide.

Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV;

gp120; C-type lectin; ICAM3; HIV entry; T cell; macrophage;

HIV infection.

Homo sapiens.

WO200164752-A2.

07-SEP-2001.

28-FEB-2001; 2001WO-US06322.

02-MAR-2000; 2000US-0517605.

(UYNI) UNIV NEW YORK STATE.

(UYNI-) UNIV NIJMEGEN.

Litman DR, Kwon D, Van Kooyk Y, Geljtenbeek T;

WPI: 2001-602565/68.

Disclosure; Page 123-124; 131pp; English.

The specification describes an antibody which is specific for an
antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN

CC or is exposed upon gp120 binding of DC-SIGN due to concomitant
 CC conformational change. DC-SIGN is a receptor that is specifically
 CC expressed on dendritic cells and facilitates infection of T lymphocytes
 CC with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin.
 CC DC-SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes)
 CC with high affinity. The antibody of the invention inhibits the trans
 CC enhancement of HIV entry into a T cell or macrophage facilitated by
 CC dendritic cells. The antibody is useful to treat or prevent HIV
 CC infection. The present sequence represents a human polypeptide.
 CC which is used in the course of the invention.

XX Sequence 342 AA;

Query Match 100.0%; Score 1794; DB 22; Length 342;
 Best Local Similarity 100.0%; Pred. No. 1.4e-180;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEHDYEDYGFSSFNDSQEHODFLQFSKVPFCMYLVFVCGLVGNSLVVISIFYH 60
 1 MAEHDYEDYGFSSFNDSQEHODFLQFSKVPFCMYLVFVCGLVGNSLVVISIFYH 60
 QY KIOSLDFVFLVNLPLADLVFVCTLPFWAYAGIHEWVGQVCKSLGITYINFTSMIL 120
 DB 61 KIOSLDFVFLVNLPLADLVFVCTLPFWAYAGIHEWVGQVCKSLGITYINFTSMIL 120
 QY 121 TCITVDRFIYVVKATKAYNOQAKRMWGKTSLLIWIISLVSPQIITYGNVFNLDKLC 180
 DB 121 TCITVDRFIYVVKATKAYNOQAKRMWGKTSLLIWIISLVSPQIITYGNVFNLDKLC 180
 QY 181 GYHDEAISTVVALTOMTLGFFPLIMIVCYVIKTLHAGGFQKRSKIIFLYWAVF 240
 DB 181 GYHDEAISTVVALTOMTLGFFPLIMIVCYVIKTLHAGGFQKRSKIIFLYWAVF 240
 QY 241 LITOMPENLMKFFIRSTHMEYAMTSFYITIMVTEALAYLRACLPVYAVSLKFRKNF 300
 DB 241 LITOMPENLMKFFIRSTHMEYAMTSFYITIMVTEALAYLRACLPVYAVSLKFRKNF 300
 QY 301 KLVKDIGCLPYLGVS HQKSEDSNKTFSASHNVEATSMFQL 342
 DB 301 KLVKDIGCLPYLGVS HQKSEDSNKTFSASHNVEATSMFQL 342

RESULT 7
 AAG67239
 ID AAG67239 standard; Protein: 342 AA.

XX AAG67239;

13-NOV-2001 (first entry)

XX Amino acid sequence of human chemokine receptor Bonzo.
 XX

KW Human: chemokine receptor: CCR11; G protein coupled receptor;
 KW inflammatory disease; Rheumatoid arthritis; inflammatory bowel disease;
 KW asthma; angiodysplasia; arteriosclerosis vascular association disease;
 KW hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon;
 KW left ventricular diastolic dysfunction; migraine; preterm labour;
 KW oesophageal spasm; ischaemic stroke; subarachnoid haemorrhage;
 KW myocardial infarction; congestive heart failure; endometritis; Bonzo;
 KW vasospasm; retinopathy; nephropathy; pulmonary vascular disease.

OS Homo sapiens.

XX WO200166598-A2.

XX 13-SEP-2001.

XX 05-MAR-2001; 2001WO-US07073.

XX 03-MAR-2000; 2000US-0186928.
 PR 03-MAR-2000; 2000US-0187231.

XX (ICOS-) ICOS CORP.
 PA

XX Gray PW, Schweickart VL, Epp A, Raport CJ, Chantry D, Steiner B;
 PI WPI: 2001-541918/60.
 XX N-PSDB: AAH77725.

XX An isolated polynucleotide encoding the chemokine receptor CCR11,
 PT useful for treating rheumatoid arthritis, inflammatory bowel disease,
 PT asthma, angiodysplasia, arteriosclerosis, cardiac arrhythmias, Raynaud's
 PT phenomenon and migraine.

XX Example 8; Page 109-110; 110pp; English.

XX The present sequence represents the human chemokine receptor Bonzo. The
 CC specification also describes the human chemokine receptor CCR11.
 CC CCR11 is a member of the G protein coupled receptor family. A CCR11
 CC polypeptide, its inhibitor, an antibody, or other modulator of CCR11
 CC expression or biological activity, is useful for treating many
 CC inflammatory diseases, for example, rheumatoid arthritis, inflammatory
 CC bowel disease, and asthma. They are also useful for treating
 CC angiodysplasia, arteriosclerosis, vascular association diseases which may
 CC include but are not limited to hypertension, angina pectoris, cardiac
 CC arrhythmias, left ventricular diastolic dysfunction, Raynaud's
 CC phenomenon, migraine, preterm labour, oesophageal spasm, ischaemic
 CC stroke, subarachnoid haemorrhage, myocardial infarction, congestive
 CC heart failure, endometritis, vasospasm, retinopathy, nephropathy, or
 CC pulmonary vascular disease.

XX Sequence 342 AA;

Query Match 100.0%; Score 1794; DB 22; Length 342;
 Best Local Similarity 100.0%; Pred. No. 1.4e-180;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEHDYEDYGFSSFNDSQEHODFLQFSKVPFCMYLVFVCGLVGNSLVVISIFYH 60
 DB 1 MAEHDYEDYGFSSFNDSQEHODFLQFSKVPFCMYLVFVCGLVGNSLVVISIFYH 60
 QY KIOSLDFVFLVNLPLADLVFVCTLPFWAYAGIHEWVGQVCKSLGITYINFTSMIL 120
 DB 61 KIOSLDFVFLVNLPLADLVFVCTLPFWAYAGIHEWVGQVCKSLGITYINFTSMIL 120
 QY 121 TCITVDRFIYVVKATKAYNOQAKRMWGKTSLLIWIISLVSPQIITYGNVFNLDKLC 180
 DB 121 TCITVDRFIYVVKATKAYNOQAKRMWGKTSLLIWIISLVSPQIITYGNVFNLDKLC 180
 QY 181 GYHDEAISTVVALTOMTLGFFPLIMIVCYVIKTLHAGGFQKRSKIIFLYWAVF 240
 DB 181 GYHDEAISTVVALTOMTLGFFPLIMIVCYVIKTLHAGGFQKRSKIIFLYWAVF 240
 QY 241 LITOMPENLMKFFIRSTHMEYAMTSFYITIMVTEALAYLRACLPVYAVSLKFRKNF 300
 DB 241 LITOMPENLMKFFIRSTHMEYAMTSFYITIMVTEALAYLRACLPVYAVSLKFRKNF 300
 QY 301 KLVKDIGCLPYLGVS HQKSEDSNKTFSASHNVEATSMFQL 342
 DB 301 KLVKDIGCLPYLGVS HQKSEDSNKTFSASHNVEATSMFQL 342

RESULT 8
 AAU04032
 ID AAU04032 standard; Protein: 342 AA.

XX AAU04032;

XX 23-OCT-2001 (first entry)

XX Human HIV translocation agent, Bonzo.

XX Human: Bonzo; human immunodeficiency virus; HIV translocating agent;
 KW CD4; BOB; Brother of Bonzo; acquired immunodeficiency syndrome;
 KW AIDS.
 XX

OS	Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
FT	Domain
FT	/label= Extracellular_domain
FT	Misc-difference
FT	53
FT	/note= "Encoded by TG"
FT	71
FT	/note= "Encoded by TC"
FT	89..102
FT	/label= Extracellular_domain
FT	106
FT	/note= "Encoded by CG"
FT	171..196
FT	/label= Extracellular_domain
FT	250..270
FT	/label= Extracellular_domain
XX	
PN	US6251582-B1.
XX	
PD	
●	16-JUL-1998; 98US-0116498.
XX	
PK	17-JUL-1997; 97US-0052827.
XX	(UYNV) UNIV NEW YORK STATE.
PA	Litman DR, Deng H, Unutmaz D, KewalRamani VN;
XX	
DR	WPI: 2001-424455/45.
DR	N-PSTDB: AAS04032.
XX	
PT	Identifying an agent for treating AIDS comprises administering a
PT	potential therapeutic agent to a cell expressing human CD4 and primate
PT	Bonzo or BOB and contacting the cell with a virus pseudotyped with an
PT	HIV envelope glycoprotein -
XX	
PS	Example 1, Fig 2C; 41pp: English.
XX	
CC	The sequence represents a novel HIV (human immunodeficiency virus)
CC	translocating agent, Bonzo. The invention relates to selecting an agent
CC	that may be used in treating acquired immunodeficiency syndrome (AIDS)
CC	comprises administering a potential therapeutic agent to a cell
CC	expressing human CD4 and primate Bonzo or BOB (Brother Of Bonzo),
CC	contacting the cell with a virus pseudotyped with an HIV envelope
CC	glycoprotein, and measuring the cell's ability to resist infection. The
CC	method is useful for selecting or identifying an agent, which can be used
CC	in treating AIDS.
X	
S	Sequence 342 AA:
●	
Query Match	100.0%; Score 1794; DB 22; Length 342;
Best Local Similarity	100.0%; Pred. No. 1,4e-180;
Matches 342; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MAEHDYHDEGFESSFNDSOEHOEDLOFSKVFPLPCMLTVFVGGLVGNLSLVYSIFRH 60
Dd	1 MAEHDYHDEGFSSFNDSOEHOEDLOFSKVFPLPCMLTVFVGGLVGNLSLVYSIFRH 60
QY	61 KLGSLTDVFLVNELDLADLVEFCCTLPFMAYAGIHEWVEFGOWACKSLLGIYTITNFYSMTLL 120
Dd	61 KLGSLTDVFLVNELDLADLVEFCCTLPFMAYAGIHEWVEFGOWACKSLLGIYTITNFYSMTLL 120
QY	121 TCGTIVDRITVVVKATKAANOAKRRTWGKVTSLLIWTISLLVSILPQIIYGNVFNMDKLIC 180
Dd	121 TCGTIVDRITVVVKATKAANOAKRRTWGKVTSLLIWTISLLVSILPQIIYGNVFNMDKLIC 180
QY	181 GYHDEALSTVVLAAQMTLGFPLPLTLMTVCYSVIITKLHLAHGGFOKRHSKTIFFVMAYF 240
Dd	181 GYHDEALSTVVLAAQMTLGFPLPLTLMTVCYSVIITKLHLAHGGFOKRHSKTIFFVMAYF 240
YY	241 LLIOMPENLMKFIRSTHWEYIAMTSEHTINWTEIAIYLRACLNDELVTAYAFVSLKFRKNFW 300

Dd		241	LTLQMPFNLMKFKIRSHHWMEYAMTSFHYIIMWTEAIALRLACMLPVLAFAVSLKFRKNFW	3000
Oy		301	KLYKDIGCLPYLGVSHPQMSSEDNSTXTSASHINVEATSMFLD	342
Dd		301	KLVKDIGCLPYLGVSHPQMSSEDNSTXTSASHINVEATSMFLD	342
			23-JUL-2001 (first entry)	
Xx			Amino acid sequence of a human Bonzo polypeptide.	
De			Bonzo; CXC chemokine receptor; inflammatory disease; cancer; infection;	
Rw			SEXCKine; spleen extracted chemokine.	
Kw			Homo sapiens.	
Os			MO200137872-A1.	
Xx			31-MAY-2001.	
Pn			22-NOV-2000; 2000MO-US32206.	
Xx			24-NOV-1999; 99US-0449437.	
Px			(MILL-) MILLENNIUM PHARM INC.	
Pa			Briskin MJ, Murphy KE, Wilbanks AM, Wu L;	
Pi			WPI: 2001-343947/36.	
Dr			N-PSDB: AAF85364.	
Xx			Identifying agents (especially antibodies) which bind to the CXC	
Pt			chemokine receptor Bonzo, and which may be used to treat e.g. cancers	
Pt			and inflammation -	
Xx			Example 1; Fig 2; 191pp; English.	
Px			The present sequence represents a human Bonzo polypeptide. Bonzo is a	
Cc			CXC chemokine receptor. The specification describes a method for	
Cc			identifying agents (especially antibodies) which bind to Bonzo and	
Cc			inhibit the binding of a ligand (especially SEXCKine (spleen extracted	
Cc			chemokine)) and the agents per se. The agents identified may be used	
Cc			for the treatment of a disorder/disease related to aberrant Bonzo	
Cc			expression and activity, such as inflammatory disease, cancers and/or	
Cc			infections (e.g. viral, bacterial and fungal infections).	
Sq			Sequence 342 AA:	
			Query Match 100.0%; Score 1794; DB 22; Length 342;	
			Best Local Similarity 100.0%; Pred. No. 1.4e-180; Indels 0; Gaps 0	
			Matches 342; Conservative 0; Mismatches 0;	
Oy		1	MAREHDHEDYGFSFNDSSQEHEODLOFSRKYFLPCMTLVVFVCGLGNLSVLVISIFYH	60
Dd		1	MAEHVDHEDYGFSSFFNDSQEEHQDFLFGRKYFLPCMTLVVFVCGLGNLSVLVISIFYH	60
Oy		61	KIOSLDLVAVNLPLADLVFCVTLPFPAAAGIHENVRGQVWCKSLGIITINFTSMIL	120
Dd		61	KIOSLDLVAVNLPLADLVFCVTLPFPAAAGIHENVRGQVWCKSLGIITINFTSMIL	120
Oy		121	TCTIVDRFLVVAKATKAYNQQAQRMTGWKYSLLIWVLSLVSIPQIIYGVNFMDKLIC	180
Dd		121	TCTIVDRFLVVAKATKAYNQQAQRMTGWKYSLLIWVLSLVSIPQIIYGVNFMDKLIC	180
Oy		181	GYNDEAISTVVALATQNTGGFLPLLTMIVCYSVIIKTLLAHAGGFQKHRSKIIFLVMAVF	240

Db 181 GHDEAISTVVLATQMTLGFPLPLTMIVCSYVIAIKTLHAAGFQKRSILKIIFLVMAVF 240
 QY 241 LLTQMPFNLMKFIRSTHMEYAMTSFHTTIIVTEAIVLRACLNPVLYAFVSLKFRKNFW 300
 Db 241 LLTQMPFNLMKFIRSTHMEYAMTSFHTTIIVTEAIVLRACLNPVLYAFVSLKFRKNFW 300
 QY 301 KLVADICGLPYLGVS HQKSSSEDSKTFSSASHNEATSMFQL 342
 Db 301 KLVADICGLPYLGVS HQKSSSEDSKTFSSASHNEATSMFQL 342

RESULT 10
 AAM97785
 ID AAM97785 standard; Protein: 342 AA.
 AC AAM97785;
 XX 21-MAY-1999 (first entry)
 PF Pig-tailed macaque HIV/SIV receptor protein Bonzo.
 KW SIV receptor; HIV receptor; Bonzo: translocation promoting agent;
 KM G protein coupled receptor; chemokine receptor; AIDS; Infection;
 XX virus transmission; pig-tailed macaque.
 OS Macaca nemestrina.
 XX
 PN WO9903888-A1.
 PD 28-JAN-1999.
 XX 17-JUL-1998; 98WO-US14857.
 PF 17-JUL-1997; 97US-0896155.
 XX 17-JUL-1997;
 PR (UYNY) UNIV NEW YORK STATE.
 XX
 PA Deng H, Kewalramani VN, Littman DR, Unutmaz D;
 PI WPI: 1999-132164/11.
 DR N-PSDB: AAX07291.
 XX
 PT New nucleic acid encoding the human translocation promoter Bonzo -
 PR used to screen for potential agents for treating acquired immune
 PT deficiency syndrome
 XX
 XX Disclosure: Page 82-83; 97pp; English.

This is the amino acid sequence of pig-tailed macaque Bonzo, a novel HIV/SIV translocation promoting agent that acts in conjunction with CD4 to serve as a receptor for the entry into a cell of a virus having a specific viral envelope glycoprotein. Bonzo is a member of the 7-transmembrane G-protein coupled receptor family, is closely related to the chemokine receptor family, and is expressed in lymphoid tissues. The invention provides the amino acid sequences (see AAM97783-88) and DNA sequences (see AAX07289-94) of human, African green monkey and pig-tailed macaque Bonzo and Bob (brother of Bonzo) translocation promoting agents. These novel receptors were identified using an expression cloning strategy. They were found to be used by particular strains of HIV-2 and M-tropic HIV-1. The invention also includes: mammalian cells transfected with Bonzo and/or Bob and human CD4, which can be used to screen potential therapeutic agents and identify ligands; antibodies to Bonzo, which can be used therapeutically, e.g. as antagonists or to target toxins or radioisotopes to HIV-permissive cells; transgenic animals; and antisense and ribozyme molecules, which may also be used therapeutically, particularly expressed from a gene therapy vector.

Sequence 342 AA:
 Query Match 96.4%; Score 1730; DB 20; Length 342;
 Best Local Similarity 95.6%; Pred. No. 8e-174;

Matches 327; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MAEHYEDYGFSSFNDSOEHDPLQESKVPICMAYVYVCGIGNSLIVISFEYH 60
 Db 1 MAEHYEDYGLNSFNDSOEHDPLQESKVPICMAYVYVCGIGNSLIVISFEYH 60
 QY 61 KLSLTQVFLVNLPLADLVFVCTLPFAVAGIHMEVGOVCKSLIGYTFNFTSMIL 120
 Db 61 KLSLTQVFLVNLPLADLVFVCTLPFAVAGIHMEVGOVCKSLIGYTFNFTSMIL 120
 QY 121 TCITVDRFIVVKKATKAYNOAKRMWGVKYSLLIWIISLVSLPQIITYGVNEMDLKIC 180
 Db 121 TCITVDRFIVVKKATKAYNOAKRMWGVKYSLLIWIISLVSLPQIITYGVNEMDLKIC 180
 QY 181 GHDEAISTVVLATQMTLGFPLPLTMIVCSYVIAIKTLHAAGFQKRSILKIIFLVMAVF 240
 Db 181 GHDEAISTVVLATQMTLGFPLPLTMIVCSYVIAIKTLHAAGFQKRSILKIIFLVMAVF 240
 QY 241 LLTQMPFNLMKFIRSTHMEYAMTSFHTTIIVTEAIVLRACLNPVLYAFVSLKFRKNFW 300
 Db 241 LLTQMPFNLMKFIRSTHMEYAMTSFHTTIIVTEAIVLRACLNPVLYAFVSLKFRKNFW 300
 QY 301 KLVADICGLPYLGVS HQKSSSEDSKTFSSASHNEATSMFQL 342
 Db 301 KLVADICGLPYLGVS HQKSSSEDSKTFSSASHNEATSMFQL 342

RESULT 11
 AAU04034
 ID AAU04034 standard; Protein: 342 AA.
 AC AAU04034;
 XX 23-OCT-2001 (first entry)
 PF Pig-tailed macaque SIV translocation agent, Bonzo.
 KW Pig-tailed macaque; Bonzo: simian immunodeficiency virus;
 KM SIV translocating agent; CD4; BOB: Brother of Bonzo;
 XX acquired immunodeficiency syndrome; AIDS; SIV; HIV.
 OS Macaca nemestrina.
 XX
 PN US6251582-B1.
 PD 26-JUN-2001.
 XX 16-JUL-1998; 98US-0116498.
 PF 17-JUL-1997; 97US-0052827.
 XX 17-JUL-1997;
 PR (UYNY) UNIV NEW YORK STATE.
 XX
 PA Littman DR, Deng H, Unutmaz D, Kewalramani VN;
 PI WPI: 2001-424455/45.
 DR N-PSDB: AAS07616.
 XX
 PT Identifying an agent for treating AIDS comprises administering a
 PT potential therapeutic agent to a cell expressing human CD4 and primate
 PT Bonzo or BOB and contacting the cell with a virus pseudotyped with an
 PT HIV envelope glycoprotein -
 XX
 PS Example 1: Column 43-46; 41pp; English.

The sequence represents a novel SIV (Simian immunodeficiency virus) translocating agent, Bonzo. The invention relates to selecting an agent that may be used in treating acquired immunodeficiency syndrome (AIDS) comprising administering a potential therapeutic agent to a cell expressing human CD4 and primate Bonzo or BOB (Brother of Bonzo), contacting the cell with a virus pseudotyped with an HIV envelope glycoprotein, and measuring the cell's ability to resist infection. The method is useful for selecting or identifying an agent, which can be used

in treating AIDS.

Sequence 342 AA; 96.4%; Score 1730; DB 22; Length 342;
Best Local Similarity 95.6%; Pred. No. 8e-174;
Matches 327; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

Query Match

1 MAEHYHDYGFSSFNDSOSEHOFLOFSKVFLEPCWLVVFCGLVGNLSLIVTSIFTH 60
| | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 MAEHDHDDYGLNFSNDSSOEBOHDFLOFRKFVLEPCMVLVFCGLVNSLIVTSIFTH 60
| | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 KLGSLFDVELNLPLADLVFVCITLFEMAYAGIHEWFQGVNCKSLIGITYINFTSMLT 120
| | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 61 KLGSLDVEFLNLPLADLVFVCITLFEMAYAGIHEWIFQGVNCKTLTGYYTINFTSMLT 120
| | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 TCTIVDRIRVVVKATKAANOAKRMWGKVSLLIWVLSLVSPQIIYGVENFDKLIC 180
| | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 121 TCTIVDRIRVVVKATKAANOAKRMWGKVLCLLIWVLSLVSPQIIYGVENFDKLIC 180
| | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 181 GYHDEALSTVLAQTMTLGFELPLLTMTVCYSVIITKLHAGFGFKHRSLKIIFLVMAVF 240
| | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 181 GHDKKEISTVLAQTMTLGFELPLAMTVCSVIIKTLLHAGFGFKHRSLKIIFLVMAVF 240
| | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 241 LITQPEFMKFIINSTHEYYAAMSFHITIMTEAIATLRACLNPLYAFVSLEKRKNFW 300
| | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 241 LLTGTPEFLVAKLISTHEYYAAMSFEHYTIIVTEAIATLRACLNPLYAFVSLEKRKNFW 300
| | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 301 KLKVDIGCLPYLGYSHOKSSEDSNKTPSASHNVETATSMFOL 342
| | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 301 KLKVDIGCLPYLGYSHOKSSEDSNKTPSASHNVETATSMFOL 342
| | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 12
AAW97784 standard; Protein; 342 AA.
ID AAW97784
XX AAW97784:
XX
DT 21-MAY-1999 (first entry)
XX
DE African green monkey HIV/SIV receptor protein Bonzo.
XX
KW SIV receptor; HIV receptor; Bonzo; translocation promoting agent;
KM G protein coupled receptor; chemokine receptor; AIDS; infection;
XX virus transmission; African green monkey.
XX
OS Cercopithecus aethiops.
XX
MO9903888-A1.
28-JAN-1999.
XX
PF 17-JUL-1998; 98WO-US14857.
XX
PR 17-JUL-1997; 97US-0896155.
XX
PA (UNYNY) UNIV NEW YORK STATE.
XX
PI Deng H, KewalRamani VN, Littman DR, Unutmaz D;
XX WPI; 1999-132164/11.
DR N-PSDB; AAX07290.
XX
PT New nucleic acid encoding the human translocation promoter Bonzo -
PT used to screen for potential agents for treating acquired Immune
XX deficiency syndrome
XX
PS Disclosure; Page 80-81; 97pp; English.
CC This is the amino acid sequence of African green monkey Bonzo, a
CC novel HIV/SIV translocation promoting agent that acts in conjunction
CC with CD4 to serve as a receptor for the entry into a cell of a virus

	CC	having specific viral envelope glycoprotein. Bonzo is a member of
	CC	the 7-transmembrane G-protein coupled receptor family, is closely
	CC	related to the chemokine receptor family, and is expressed in
	CC	lymphoid tissues.
	CC	The invention provides the amino acid sequences
	CC	(see AA097783-88) and DNA sequences (see AA07289-94) of human,
	CC	African green monkey and pig-tailed macaque Bonzo and Bob (brother
	CC	of Bonzo) translocation promoting agents. These novel receptors
	CC	were identified using an expression cloning strategy. They were
	CC	found to be used by particular strains of HIV-2 and M-tropic HIV-1.
	CC	The invention also includes: mammalian cells transfected with Bonzo
	CC	and/or Bob and human CD4, which can be used to screen potential
	CC	therapeutic agents and identify ligands; antibodies to Bonzo, which
	CC	can be used therapeutically, e.g., as antagonists or to target
	CC	toxins or radiolabels to HIV-permissive cells; transgenic
	CC	animals; and antisense and ribozyme molecules, which may also be
	CC	used therapeutically, particularly expressed from a gene therapy
	CC	vector.
XX	XX	
SQ	Sequence	342 AA;
	Query Match	95.7%; Score 1717; DB 20; Length 342;
	Best Local Similarity	95.3%; Pred. No. 1.9e-172;
	Matches	326; Conservative 9; Mismatches 7; Indels 0; Gaps
OY	1 MAEHYHEDYGESSEFNDSOEHOQLDFGSKVFLPCMYLVFVCGLVGNLSVLVISIFPH	60
Dd	1 MAEYDHEDNGEFNSFNDSOEHOQLDFGSKVFLPCMYLVFVCGLVGNLSVLVISIFPH	60
OY	61 KLOSLNDVFVNPLDLADLVEVCTLPFWAAGIHENWFGGWCKSLIGITINFTYSMLT	12
Dd	61 KLOSLNDVFVNPLDLADLVEVCTLPFWAAGIHENWFGGWCKTLGITINFTYSMLT	12
OY	121 TCIIVDRFIYVVKATRAYNOQAAMTWGKVTSLIINVISLVSIPDIIGNVFNLDKLIC	18
Dd	121 TCITVDRFIYVVKAFRAYNOQAAMKWGVICLLIINVISLVSIPDIIGNVFNLDKLIC	18
OY	181 GYHDEASTVVALTOMTGFEPLLMIVCYSIITKLHHAGGFOKHRSLKIIFVMNVF	24
Dd	181 GYHDEESTVVALTOMTGFEPLLMIVCYSVIITKLHHAGGFOKHRSLKIIFVMNVF	24
OY	241 LLTQMPELNKKFIRSTHWEYIAMSFPHYIMVTEAIAYLRACILNPVLAFFVSLKFRKNWF	30
Dd	241 LLTQEPENLVKRLRSHWEYIAMSFPHYITITEAIALYLRACILNPVLAFAVSLKRRKNWF	30
OY	301 KLYKDIGCLPYLGVS HQMKSSSEDNKTFSASHNVEATSMFOL	342
Dd	301 KLWKDIGCLPYLGVS HQMKSSSEDNKTFSASHNVEATSMFOL	342
RESULT 13		
ID	AAU04033 standard; Protein; 342 AA.	
XX	AAU04033:	
DT	23-OCT-2001 (first entry)	
DE	Green monkey SIV translocation agent, Bonzo.	
KM	Monkey; Bonzo; simian immunodeficiency virus; SIV translocating agent;	
KW	CD4; BOB; Brother of Bonzo; acquired immunodeficiency syndrome;	
KW	AIDS; SIV; HIV.	
OS	Cercopithecus aethiops.	
PN	US6251582-B1.	
PD	26-JUN-2001.	
PF	16-JUL-1998; 98US-0116498.	
PR	17-JUL-1997; 97US-0052827.	

PA (UYNV) UNIV NEW YORK STATE.

XX Littman DR, Deng H, Unutmaz D, Kewalramani VN;

XX WPI: 2001-424455/45.

DR N-PSDB: AAS07615.

XX Identifying an agent for treating AIDS comprises administering a
XX potential therapeutic agent to a cell expressing human CD4 and primate
XX Bonzo or BOB and contacting the cell with a virus pseudotyped with an
XX HIV envelope glycoprotein.

PS Example 1; Column 41-42: 41pp; English.

XX The sequence represents a novel HIV (Simian immunodeficiency virus)
XX translocating agent, Bonzo. The invention relates to selecting an agent
XX that may be used in treating acquired immunodeficiency syndrome (AIDS)
XX comprising administering a potential therapeutic agent to a cell
XX expressing human CD4 and primate Bonzo or BOB (Brother Of Bonzo),
XX contacting the cell with a virus pseudotyped with an HIV envelope
XX glycoprotein, and measuring the cell's ability to resist infection. The
XX method is useful for selecting or identifying an agent, which can be used
XX in treating AIDS.

CC Sequence 342 AA;

Query Match 95.7%; Score 1717; DB 22; Length 342;

Best Local Similarity 95.3%; Pred. No. 1.9e-172; Matches 326; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAEHYHEDYGFSSFNDSOEHODFLOFSKVFLEPCMYLVFVCGLVGNSLVVISIFYH 60
DB 1 MAEYHYEDNGFNFSNDSOEHODFLOFSKVFLEPCMYLVFVCGLVGNSLVVISIFYH 60
QY 61 KLOSLDFVFLNPLADLVFVCTLPFAVAGIHEWFGVQWCKSLGITYINFTSMIL 120
DB 61 KLOSLDFVFLNPLADLVFVCTLPFAVAGIHEWFGVQWCKSLGITYINFTSMIL 120
QY 121 TCITVDFRIYVVKATKAYNOQAKRMWGKVTSLIMVTSLSVSPQIITGVNFDKILIC 180
DB 121 TCITVDFRIYVVKATKAYNOQAKRMWGKVTSLIMVTSLSVSPQIITGVNFDKILIC 180
QY 181 GYHDEAISTVVLATQMTLGFELPLITMIVCYSVIIKTLHAGGFQKHRSKLIIFLVMAVF 240
DB 181 GYHDEAISTVVLATQMTLGFELPLITMIVCYSVIIKTLHAGGFQKHRSKLIIFLVMAVF 240
QY 241 LITQMPENLMKFIKSTHMEYVAMTSFHTITMTEAIALRACLNVPVLYAFVSLKFRKNF 300
DB 241 LITQMPENLMKFIKSTHMEYVAMTSFHTITMTEAIALRACLNVPVLYAFVSLKFRKNF 300
QY 301 KLVKDIGCLPYLGVSQWKSSEDNSKTFSSASHNVEATSMFOL 342
DB 301 KLVKDIGCLPYLGVSQWKSSEDNSKTFSSASHNVEATSMFOL 342

RESULT 14
AAY23825

ID AAY23825 standard; Protein: 351 AA.

XX AAY23825;

XX 15-SEP-1999 (first entry)

XX A7 times membrane penetrating type receptor protein ET60.

XX 7 times membrane-penetrating type receptor protein; ET60;

XX leukocyte function; control; drug.

XX Unidentified.

XX JP1155573-A.

XX 15-JUN-1999.

XX 27-NOV-1997; 97JP-0325823.

XX 27-NOV-1997; 97JP-0325823.

XX (ASAH) ASAH KASEI KOGYO KK.

XX WPI: 1999-398070/34.

DR N-PSDB: AAX86032.

XX New 7 times membrane-penetrating type receptor protein ET60 - useful
XX for detecting drug controlling function of leukocyte

PS Claim 1; Page 17-18; 20pp; Japanese.

XX The present sequence represents a 7 times membrane-penetrating type
XX receptor protein ET60. The 7 times membrane-penetrating type
XX receptor protein ET60 can be used for detecting a drug controlling
XX the function of leukocyte.

CC Sequence 351 AA;

Query Match 74.2%; Score 1332; DB 20; Length 351;

Best Local Similarity 75.2%; Pred. No. 7.5e-132; Matches 258; Conservative 36; Mismatches 47; Indels 2; Gaps 1;

QY 2 AEHYHEDYGFSSFNDS--QEHODFLOFSKVFLEPCMYLVFVCGLVGNSLVVISIFY 59
DB 9 ALYGHYEGDWLFRNSSDNSOENKRFLEKFEVLPVYLVFVFGLVGNSLVVISIFY 68
QY 60 HKLOSLDFVFLNPLADLVFVCTLPFAVAGIHEWFGVQWCKSLGITYINFTSMIL 119
DB 69 OKLRTLDVFLNPLADLVFVCTLPFAVAGIHEWFGVQWCKSLGITYINFTSMIL 128
QY 120 LTCITVDFRIYVVKATKAYNOQAKRMWGKVTSLIMVTSLSVSPQIITGVNFDKIL 179
DB 129 LTCITVDFRIYVVKATKAYNOQAKRMWGKVTSLIMVTSLSVSPQIITGVNFDKIL 188
QY 180 GYHDEAISTVVLATQMTLGFELPLITMIVCYSVIIKTLHAGGFQKHRSKLIIFLVMAVF 239
DB 189 GYHDEAISTVVLATQMTLGFELPLITMIVCYSVIIKTLHAGGFQKHRSKLIIFLVMAVF 248
QY 240 FLITQMPENLMKFIKSTHMEYVAMTSFHTITMTEAIALRACLNVPVLYAFVSLKFRKNF 299
DB 249 FLITQMPENLMKFIKSTHMEYVAMTSFHTITMTEAIALRACLNVPVLYAFVSLKFRKNF 308
QY 300 WKLVKDIGCLPYLGVSQWKSSEDNSKTFSSASHNVEATSMFOL 342
DB 309 WKLVKDIGCLPYLGVSQWKSSEDNSKTFSSASHNVEATSMFOL 351

RESULT 15
AAM70001

ID AAM70001 standard; Protein: 302 AA.

XX AAM70001;

XX 20-OCT-1998 (first entry)

XX Rodent chemokine receptor 94ID12 amino acid sequence.

XX Chemokine; primate; human; rodent; chemokine receptor; asthma;

XX inflammatory response; immune response; leukocyte migration; GPCR;

XX leukocyte adhesion; chemotactant; modulation; antiviral response;

XX cellular morphology modification response; G-protein coupled receptor;

XX phospholipase A2; lipid turnover; abnormal proliferation; regeneration;

XX atrophy; 94ID12.

XX Mus sp.

XX WO9832858-A2.

XX 30-JUL-1998.

OY 241 LITOMPENLMKFIKSTHWEYAMTSFHYTIWTEAIAIYLRACLNPLVLAFAVSLKFRKNFW 300
DB 241 LITOMPENLMKFIKSTHWEYAMTSFHYTIWTEAIAIYLRACLNPLVLAFAVSLKFRKNFW 300
OY 301 KLVKDIGCLPYLGVSHPKSSSEDSNKTFSASHNVEATSMFOL 342
DB 301 KLVKDIGCLPYLGVSHPKSSSEDSNKTFSASHNVEATSMFOL 342

RESULT 2

US-09-852-156-2
Sequence 2, Application US/09852156
Patent No. US20020076694A1

GENERAL INFORMATION:

APPLICANT: Littman, Dan R.

Deng, Hongkui

Unutmaz, Derya

Ramani, Vineet N.K.

TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF
IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES
THEREOF

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th

FLOOR

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/852,156

FILING DATE: 09-May-2001

CLASSIFICATION: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 342 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHEICAL: NO

ORGANISM: Homo sapiens

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-852-156-2

Query Match 100.0%; Score 1794; DB 10; Length 342;

Best Local Similarity 100.0%; Pred. No. 9.8e-144;

Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAEHDYHEDYGFSSFNDSOEHDPLQFSKVFPLPCMYLVVFCGLVNSLVYISIFYH 60

DB 1 MAEHDYHEDYGFSSFNDSOEHDPLQFSKVFPLPCMYLVVFCGLVNSLVYISIFYH 60

OY 61 KLSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWFGQVWCKSLGITYINFTSMIL 120

DB 61 KLSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWFGQVWCKSLGITYINFTSMIL 120

OY 121 TCITVDRIYVVKATKAYNOQAKRTWCKVTSLLIWLISLVSLPQIIYGVNPLDKLIC 180
DB 121 TCITVDRIYVVKATKAYNOQAKRTWCKVTSLLIWLISLVSLPQIIYGVNPLDKLIC 180
OY 181 GYHDEAISTVLAQMTLGFPLPLTMIVCVSVIITKLLHAGGFOKRSKLIIFLVAVF 240
DB 181 GYHDEAISTVLAQMTLGFPLPLTMIVCVSVIITKLLHAGGFOKRSKLIIFLVAVF 240
OY 241 LITOMPENLMKFIKSTHWEYAMTSFHYTIWTEAIAIYLRACLNPLVLAFAVSLKFRKNFW 300
DB 241 LITOMPENLMKFIKSTHWEYAMTSFHYTIWTEAIAIYLRACLNPLVLAFAVSLKFRKNFW 300
OY 301 KLVKDIGCLPYLGVSHPKSSSEDSNKTFSASHNVEATSMFOL 342
DB 301 KLVKDIGCLPYLGVSHPKSSSEDSNKTFSASHNVEATSMFOL 342

RESULT 3

US-09-940-063-2

Sequence 2, Application US/09940063

Patent No. US20020090657A1

GENERAL INFORMATION:

APPLICANT: Briskin, Michael J.

APPLICANT: Murphy, Kristine E.

APPLICANT: Wilbanks, Alyson M.

APPLICANT: Wu, Lijun

TITLE OF INVENTION: No. US20020090657A1el Antibodies and ligands for "Bonzo"

FILE REFERENCE: 1855,1070-000

CURRENT APPLICATION NUMBER: US/09/940,063

PRIOR FILING DATE: 2001-08-27

PRIOR APPLICATION NUMBER: 09/449,437

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 342

TYPE: PRT

ORGANISM: Homo sapiens

US-09-940-063-2

Query Match 100.0%; Score 1794; DB 10; Length 342;

Best Local Similarity 100.0%; Pred. No. 9.8e-144;

Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAEHDYHEDYGFSSFNDSOEHDPLQFSKVFPLPCMYLVVFCGLVNSLVYISIFYH 60

DB 1 MAEHDYHEDYGFSSFNDSOEHDPLQFSKVFPLPCMYLVVFCGLVNSLVYISIFYH 60

OY 61 KLSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWFGQVWCKSLGITYINFTSMIL 120

DB 61 KLSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWFGQVWCKSLGITYINFTSMIL 120

OY 121 TCITVDRIYVVKATKAYNOQAKRTWCKVTSLLIWLISLVSLPQIIYGVNPLDKLIC 180

DB 121 TCITVDRIYVVKATKAYNOQAKRTWCKVTSLLIWLISLVSLPQIIYGVNPLDKLIC 180

OY 241 LITOMPENLMKFIKSTHWEYAMTSFHYTIWTEAIAIYLRACLNPLVLAFAVSLKFRKNFW 300

DB 241 LITOMPENLMKFIKSTHWEYAMTSFHYTIWTEAIAIYLRACLNPLVLAFAVSLKFRKNFW 300

OY 301 KLVKDIGCLPYLGVSHPKSSSEDSNKTFSASHNVEATSMFOL 342

DB 301 KLVKDIGCLPYLGVSHPKSSSEDSNKTFSASHNVEATSMFOL 342

RESULT 4

US-09-852-156-6

Sequence 6, Application US/09852156

Patent No. US20020076694A1
GENERAL INFORMATION:
APPLICANT: Littman, Dan R.
Deng, Hongkui
Unutmaz, Derya
Ramanl, Vineet N.K.
TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF
IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES
THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/852,156
FILING DATE: 09-May-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-009NCIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
FAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Pigtail macaque
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
-09-852-156-6
Query Match 96.4%; Score 1730; DB 10; Length 342;
Best Local Similarity 95.6%; Pred. No. 2.5e-138;
Matches 327; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

1 MAEDHYHEDYGFSSNDSSQEBHODFLQFSKVFPCMYLVVFCGLVNSLVVISIYH 60
1 MAEDHYHEDYGLNSFNSDSEHODFLQFRVVFPCMYLVVFCGLVNSLVVISIYH 60
61 KLOSLTDVFLNPLADLVFVCTLPFMAVAGIHEWFEQVWCKSLGITYTINFTSMIL 120
61 KLOSLTDVFLNPLADLVFVCTLPFMAVAGIHEWFEQVWCKSLGITYTINFTSMIL 120
61 KLOSLTDVFLNPLADLVFVCTLPFMAVAGIHEWFEQVWCKSLGITYTINFTSMIL 120
121 TCITVDRTIVVKKATKAYNOAKRMTGKVTSLTIWISLVSLPQIITYGNVFNLDKILC 180
121 TCITVDRTIVVKKATKAYNOAKRMTGKVTSLTIWISLVSLPQIITYGNVFNLDKILC 180
121 TCITVDRTIVVKKATKAYNOAKRMTGKVTSLTIWISLVSLPQIITYGNVFNLDKILC 180
181 GYHDEAISTVVALQMTLGFELPLMTVCYSVVIKTLHAAGGFOKHSKLIIFLVMAVF 240
181 GYHDEAISTVVALQMTLGFELPLMTVCYSVVIKTLHAAGGFOKHSKLIIFLVMAVF 240
241 LITQPFMLKMFIRSTHMEYAMTSFHTIWTETAIATLRACLNVLAFASLKRKNFW 300
241 LITQPFMLKMFIRSTHMEYAMTSFHTIWTETAIATLRACLNVLAFASLKRKNFW 300
301 KLVKDIGCLPYLGVSHQWSSBDNSKTFPSASHNVEATSMFOL 342

DB 301 KLVKDIGCLPYLGVSHQWSSBDNSKTFPSASHNVEATSMFOL 342
RESULT 5
US-09-852-156-4
Sequence 4, Application US/09852156
Patent No. US20020076694A1
GENERAL INFORMATION:
APPLICANT: Littman, Dan R.
Deng, Hongkui
Unutmaz, Derya
Ramanl, Vineet N.K.
TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF
IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USE
THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/852,156
FILING DATE: 09-May-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-009NCIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
FAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: African Green Monkey
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
-09-852-156-4
Query Match 95.7%; Score 1717; DB 10; Length 342;
Best Local Similarity 95.3%; Pred. No. 3.1e-137;
Matches 326; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

1 MAEDHYHEDYGFSSNDSSQEBHODFLQFSKVFPCMYLVVFCGLVNSLVVISIYH 60
1 MAEDHYHEDYGNFNSDSEHODFLQFSKVFPCMYLVVFCGLVNSLVVISIYH 60
61 KLOSLTDVFLNPLADLVFVCTLPFMAVAGIHEWFEQVWCKSLGITYTINFTSMIL 120
61 KLOSLTDVFLNPLADLVFVCTLPFMAVAGIHEWFEQVWCKSLGITYTINFTSMIL 120
61 KLOSLTDVFLNPLADLVFVCTLPFMAVAGIHEWFEQVWCKSLGITYTINFTSMIL 120
121 TCITVDRTIVVKKATKAYNOAKRMTGKVTSLTIWISLVSLPQIITYGNVFNLDKILC 180
121 TCITVDRTIVVKKATKAYNOAKRMTGKVTSLTIWISLVSLPQIITYGNVFNLDKILC 180
121 TCITVDRTIVVKKATKAYNOAKRMTGKVTSLTIWISLVSLPQIITYGNVFNLDKILC 180
181 GYHDEAISTVVALQMTLGFELPLMTVCYSVVIKTLHAAGGFOKHSKLIIFLVMAVF 240
181 GYHDEAISTVVALQMTLGFELPLMTVCYSVVIKTLHAAGGFOKHSKLIIFLVMAVF 240

Db 181 GYHDEISTVVLATQMTLGFLLPLAMTVCSVIKTLHAGGFOKRSKTIIFLVAVF 240
Qy 241 LITQMPFNLMKFIKSTHWEYAMTSFHYTIWTEAIAVLRAQLPVLAVPSLKRKNFW 300
Db 241 LITQMPFNLMKFIKSTHWEYAMTSFHYTIWTEAIAVLRAQLPVLAVPSLKRKNFW 300
Qy 301 KLVVDIGCLPVLGVSQKSSSEDSKTSASHNVEATSMFOL 342
Db 301 KLVVDIGCLPVLGVSQKSSSEDSKTSASHNVEATSMFOL 342
RESULT 6
US-10-225-567A-390
Sequence 390, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: Lifespan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burner, Glenn C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
NUMBER OF SEQ ID NOS: 2392
SOFTWARE: PatentIn version 3.1
SEQ ID NO 390
LENGTH: 374
TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-390
Query Match 34.4%, Score 617; DB 9; Length 374;
Best Local Similarity 36.3%, Pred. No. 2e-44;
Matches 135; Conservative 77; Mismatches 116; Indels 44; Gaps 9;
Qy 5 DYHEDYGFSSFNDSOEHODF-----QFSKVFLLPCMYLVFVCGLVGNSLVAVIS 56
Db 13 DSSBDY-FVSVNTSYVSVDSEMLCSLQEVROFSLFVPLVSLICVEGLGNILVITFE 71
Qy 57 IFYHKLQSLTDFVLNPLADLVFVCTLPFWAVA-GIHEWEGOVCKSLIGITYTINPT 115
Db 72 AFYKASMTDVLNMAIDILFVLDPFVAVSHAGAWFSNATCKLKGITAINNC 131
Qy 116 SMLITCTVDREFIVVAKATRAYNOQAKRMWGKVTSLIWLIVSLVSLPQIIYGNFNL 175
Db 132 GMLLTCTISMDRYIAIQAATKSPRLRSRSLPRKTIICLVWGLVITSSSFVENOKYNT 191
Qy 176 D-KIICGYHDEAIS-----TVVLATQMTLGFLLPLAMTVCSVIKTLHAGGFOKHR 228
Db 192 QGSVDCPEKYQVTESEPIRMKMLLGLLELFGFFIPLMFEMFCYFIVYKTVLQAONSKRK 251
Qy 229 SLKTIIFVMAVFLITQMPFNLM-----KFIKSTHWEYAMTSFHYTIWTEAIAVL 279
Db 252 AIRITIAVVLVFLACQIPHNANVLLVTANLGNKMRSCOSE-----KLIGTYTIEVAFL 307
Qy 280 RACINPVLYAVFVSLKFRKNFKLVKDIGCLPYLGVSQKSSSEDSKTSASHNVEATSMFOL 330
Db 308 HCCINPVLYAVFVSLKFRKNFKLVKDIGCLPYLGVSQKSSSEDSKTSASHNVEATSMFOL 362
Qy 331 SHNVEATSMFOL 342
Db 363 TADNDNASSFTM 374
RESULT 7
US-09-966-755-2
Sequence 2, Application US/09966755
Publication No. US20030022238A1
GENERAL INFORMATION:
APPLICANT: Andrew, David P.

APPLICANT: Zabel, Brian A.
APPLICANT: Ponath, Paul D.
TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
FILE REFERENCE: IKS98-16
CURRENT APPLICATION NUMBER: US/09/966,755
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/09/266,464
PRIOR FILING DATE: 1999-03-11
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 357
TYPE: PRT
ORGANISM: Homo sapiens
US-09-966-755-2
Query Match 34.1%, Score 612; DB 9; Length 357;
Best Local Similarity 36.3%, Pred. No. 5.1e-44;
Matches 123; Conservative 82; Mismatches 100; Indels 34; Gaps 8;
Qy 8 EDYGFSSFNDSOEHODF-----LQFSKVFLLPCMYLVFVCGLVGNSLVAVIS 55
Db 3 DDYGF--SESTISSMEDYVNFNTDFYCKKNVROFASHFLPPLVLYFVIGALGSLVILV 60
Qy 56 SIYHKLQSLTDFVLNPLADLVFVCTLPFWAVAGIHEWEGOVCKSLIGITYTINPT 115
Db 61 YWYCTRVKTYTMDMLNLAIDLFLVLPFWAIAADQMKFQFMCKVAVSMYKMFYS 120
Qy 116 SMLITCTVDREFIVVAKATRAYNOQAKRMWGKVTSLIWLIVSLVSLPQIIYGNFNL 175
Db 121 CVLLIMCISVDRTYIAIQAATKSPRLRSRSLPRKTIICLVWGLVITSSSFVENOKYNT 180
Qy 176 DKL-ICGY---HDEA--ISTVVLATQMTLGFLLPLAMTVCSVIKTLHAGGFOKRS 229
Db 181 SGALICMNVPSDSSTKLKSAVLKYLIGFPLFVVMACCYTIITHTLQAKSSSKHA 240
Qy 230 LKTIIFVMAVFLITQMPFNLMKFIKSTHWEYAM-----TSFHYTIWTEAIAVLRA 281
Db 241 LKVTITVLYVFLVLSQFPYNCILIVOTI--DAYAMFISNCASVTMIDICFOVOTIAFFHS 298
Qy 282 CLNPLVLYAVFVSLKFRKNFKLVKDIGCLPYLGVSQKSSSEDSKTSASHNVEATSMFOL 320
Db 299 CLNPLVLYAVFVGERRRDLVTKLNLGCTIS---QAQWVS 333
RESULT 8
US-10-251-385-24
Sequence 24, Application US/10251385
Publication No. US20030105292A1
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Protein-Coupled
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/10/251,385
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 357
TYPE: PRT
ORGANISM: Homo sapiens
US-10-251-385-24
Query Match 34.1%, Score 612; DB 9; Length 357;
Best Local Similarity 36.3%, Pred. No. 5.1e-44;
Matches 123; Conservative 82; Mismatches 100; Indels 34; Gaps 8;


```
OY      8 EDYGFSSFNDSOEHODF-----LOFSKYFLPCMYLVFVCGLVGNSLVLYI 55
      3 DDYG--SESTSSMEDYVNFNTDFYCEKNNVROFASHFLPLPLYMLFVIGALGNSLVLY 60
Db
OY      56 SIFPHKQSLDVLVNLPLADLVFVCTLPFWMAAGIHEWFGOVCKSLGITYINFT 115
      61 YWCTRVKVTMTDMLNLAIADLFLVTLFPWMAAADQMKFQFMCKVNSMYKMFYS 120
Db
OY      116 SMLITCTVDREFIVVATKAYNOAKRMVGTSLIIVISLVSLPOLIIGNVNL 175
      121 CVLLIMCISVDRTYIAQAMRAHTRERKRLYSKWCTIIVLAAALCIPILISQIKEE 180
Db
OY      176 DKL-ICGY--HDEA--ISTVVLATQMTLGFELPLTMIVCYSVIITKLHAGGFQKHS 229
      181 SGAIACIMVYPSDESTKLKSAVLLIKVLGFFLPFVWVACCTYIIHTLQAKKSSKHKA 240
Db
OY      230 LKIIFLVAVFLTLQMPFNLMKFIKSTHWEYAM-----TSFHTIMVTEAIVYRA 281
      241 LKVTITVTVFVLSQFPYNCILVQTI--DAYAMFISNCVSTNIDICFQVOTIAPFHS 298
OY
Db      282 CLNPVLYAFVSLKFRKNFMKLVKIDICLPYLGVSQWKS 320
      299 CLNPVLYFVGERRRDLVKTLLKMLGCLIS---QAQWVS 333
```

RESULT 9

```
US-10-225-567A-241
; Sequence 241, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 241
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
10-225-367A-241
```

```
Query Match      34.1%; Score 612; DB 9; Length 357;
Best Local Similarity 36.3%; Pred. No. 5,1e-44;
Matches 123; Conservative 82; Mismatches 100; Indels 34; Gaps 8;
```

```
OY      8 EDYGFSSFNDSOEHODF-----LOFSKYFLPCMYLVFVCGLVGNSLVLYI 55
      3 DDYG--SESTSSMEDYVNFNTDFYCEKNNVROFASHFLPLPLYMLFVIGALGNSLVLY 60
Db
OY      56 SIFPHKQSLDVLVNLPLADLVFVCTLPFWMAAGIHEWFGOVCKSLGITYINFT 115
      61 YWCTRVKVTMTDMLNLAIADLFLVTLFPWMAAADQMKFQFMCKVNSMYKMFYS 120
Db
OY      116 SMLITCTVDREFIVVATKAYNOAKRMVGTSLIIVISLVSLPOLIIGNVNL 175
      121 CVLLIMCISVDRTYIAQAMRAHTRERKRLYSKWCTIIVLAAALCIPILISQIKEE 180
Db
OY      176 DKL-ICGY--HDEA--ISTVVLATQMTLGFELPLTMIVCYSVIITKLHAGGFQKHS 229
      181 SGAIACIMVYPSDESTKLKSAVLLIKVLGFFLPFVWVACCTYIIHTLQAKKSSKHKA 240
Db
OY      230 LKIIFLVAVFLTLQMPFNLMKFIKSTHWEYAM-----TSFHTIMVTEAIVYRA 281
      241 LKVTITVTVFVLSQFPYNCILVQTI--DAYAMFISNCVSTNIDICFQVOTIAPFHS 298
Db
```

```
OY      282 CLNPVLYAFVSLKFRKNFMKLVKIDICLPYLGVSQWKS 320
      299 CLNPVLYFVGERRRDLVKTLLKMLGCLIS---QAQWVS 333
Db
```

RESULT 10

```
US-09-903-377-2
; Sequence 2, Application US/09903377
; Patent No. US20020116727A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CHEMOKINE
; FILE REFERENCE: R-365
; CURRENT APPLICATION NUMBER: US/09/903,377
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/217,255
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/221,483
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/262,113
; PRIOR FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Targeting vector
US-09-903-377-2
```

```
Query Match      34.1%; Score 612; DB 10; Length 357;
Best Local Similarity 36.3%; Pred. No. 5,1e-44;
Matches 123; Conservative 82; Mismatches 100; Indels 34; Gaps 8;
```

```
OY      8 EDYGFSSFNDSOEHODF-----LOFSKYFLPCMYLVFVCGLVGNSLVLYI 55
      3 DDYG--SESTSSMEDYVNFNTDFYCEKNNVROFASHFLPLPLYMLFVIGALGNSLVLY 60
Db
OY      56 SIFPHKQSLDVLVNLPLADLVFVCTLPFWMAAGIHEWFGOVCKSLGITYINFT 115
      61 YWCTRVKVTMTDMLNLAIADLFLVTLFPWMAAADQMKFQFMCKVNSMYKMFYS 120
Db
OY      116 SMLITCTVDREFIVVATKAYNOAKRMVGTSLIIVISLVSLPOLIIGNVNL 175
      121 CVLLIMCISVDRTYIAQAMRAHTRERKRLYSKWCTIIVLAAALCIPILISQIKEE 180
Db
OY      176 DKL-ICGY--HDEA--ISTVVLATQMTLGFELPLTMIVCYSVIITKLHAGGFQKHS 229
      181 SGAIACIMVYPSDESTKLKSAVLLIKVLGFFLPFVWVACCTYIIHTLQAKKSSKHKA 240
Db
OY      230 LKIIFLVAVFLTLQMPFNLMKFIKSTHWEYAM-----TSFHTIMVTEAIVYRA 281
      241 LKVTITVTVFVLSQFPYNCILVQTI--DAYAMFISNCVSTNIDICFQVOTIAPFHS 298
OY
Db      282 CLNPVLYAFVSLKFRKNFMKLVKIDICLPYLGVSQWKS 320
      299 CLNPVLYFVGERRRDLVKTLLKMLGCLIS---QAQWVS 333
```

RESULT 11

```
US-09-952-385-2
; Sequence 2, Application US/09952385
; Patent No. US20020119504A1
; GENERAL INFORMATION:
; APPLICANT: Andrew, David P.
; APPLICANT: Zabel, Brian A.
; APPLICANT: Ponath, Paul D.
; TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
; FILE REFERENCE: LWS98-16
; CURRENT APPLICATION NUMBER: US/09/952,385
```

CURRENT FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: 09/266,464
PRIOR FILING DATE: 1999-03-11
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FASTSEQ for Windows version 3.0
SEQ ID NO 2
LENGTH: 357
TYPE: PRT
ORGANISM: Homo sapiens
US-09-952-385-2

Query Match 34.1%; Score 612; DB 10; Length 357;
Best Local Similarity 36.3%; Pred. No. 5,1e-44;

Matches 123; Conservative 82; Mismatches 100; Indels 34; Gaps 8;

QY 8 EDYGFSSFNDSOEHOE-----LQFSKVFPCMYLVFVCGVLSVLYI 55
DB 3 DDYG--SESTSSMEDYVNFNFTDFYCEKNNVROFASHFLPPLVYLVFVGLNSVLYI 60
QY 56 SIEFHKLQSLDVLVNLPLADLVFVCTLPFWAYAGIHENWFGVGMCKSLGITYINFT 115
DB 61 YWCTRVKTMMDMLNLAIADLFLVLPFWALAAADQMFQTFMCKVNSMYKMFYS 120
QY 116 SMLITCTVDFRYVYVATKAYNOQAKRMWGVTSLLIWLISLVSPQIIGNVNL 175
DB 121 CVLLIMCISVDRYTAIQAMRAHWTREKRLYSKMVCTIWLAAALCIPILISQKEE 180
QY 176 DKL-ICGY--HDEA--ISTVLATQMTLGFELPLTMIVCYSVIIRKLHAGFQKHRS 229
DB 181 SGAIACIMVWPSDESTKLSAVLTKVLGFEPLFVWACCYTIILHLLIOAKSSKHKA 240
QY 230 LKIFILVAVFLLQMPENLKFIRSTHWEYAM-----TSFHTYIMTEAIVLRA 281
DB 241 LKVTITVLVAVLSQFPNCLILVQTI--DAVAFISNCASVTINDICFOVTQTIAPFHS 298
QY 282 CLNPVLYAFVSLKFRKNWKLVDIGCLPYLGVSQHKRS 320
DB 299 CLNPVLYFVGERFRRLDVLTKNLGCTS-----QAQWVS 333

RESULT 12
US-10-000-759A-2
Sequence 2, Application US/10000759A
Patent No. US2002014191A1
GENERAL INFORMATION:

APPLICANT: Andrew, David P.
APPLICANT: Zabel, Brian A.
APPLICANT: Ponath, Paul D.
TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
TITLE OF INVENTION: IDENTIFYING MODULATORS OF GPR-9-6 FUNCTION
FILE REFERENCE: 1855, 1064-003
CURRENT APPLICATION NUMBER: US/10/000,759A
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: US/09/522,752
PRIOR FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: US 09/266,464
PRIOR FILING DATE: 1999-03-11
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows version 4.0
SEQ ID NO 2
LENGTH: 357
TYPE: PRT
ORGANISM: Homo sapiens
US-10-000-759A-2

Query Match 34.1%; Score 612; DB 12; Length 357;
Best Local Similarity 36.3%; Pred. No. 5,1e-44;

Matches 123; Conservative 82; Mismatches 100; Indels 34; Gaps 8;

QY 8 EDYGFSSFNDSOEHOE-----LQFSKVFPCMYLVFVCGVLSVLYI 55
DB 3 DDYG--SESTSSMEDYVNFNFTDFYCEKNNVROFASHFLPPLVYLVFVGLNSVLYI 60

QY 56 SIEFHKLQSLDVLVNLPLADLVFVCTLPFWAYAGIHENWFGVGMCKSLGITYINFT 115
DB 61 YWCTRVKTMMDMLNLAIADLFLVLPFWALAAADQMFQTFMCKVNSMYKMFYS 120
QY 116 SMLITCTVDFRYVYVATKAYNOQAKRMWGVTSLLIWLISLVSPQIIGNVNL 175
DB 121 CVLLIMCISVDRYTAIQAMRAHWTREKRLYSKMVCTIWLAAALCIPILISQKEE 180
QY 176 DKL-ICGY--HDEA--ISTVLATQMTLGFELPLTMIVCYSVIIRKLHAGFQKHRS 229
DB 181 SGAIACIMVWPSDESTKLSAVLTKVLGFEPLFVWACCYTIILHLLIOAKSSKHKA 240
QY 230 LKIFILVAVFLLQMPENLKFIRSTHWEYAM-----TSFHTYIMTEAIVLRA 281
DB 241 LKVTITVLVAVLSQFPNCLILVQTI--DAVAFISNCASVTINDICFOVTQTIAPFHS 298
QY 282 CLNPVLYAFVSLKFRKNWKLVDIGCLPYLGVSQHKRS 320
DB 299 CLNPVLYFVGERFRRLDVLTKNLGCTS-----QAQWVS 333

RESULT 13
US-10-251-385-74
Sequence 74, Application US/10251385
Publication No. US20030105292A1
GENERAL INFORMATION:

APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human
TITLE OF INVENTION: Protein-Coupled
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/10/251,385
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
SEQ ID NO 74
LENGTH: 378
TYPE: PRT
ORGANISM: Homo sapiens
US-10-251-385-74

Query Match 33.9%; Score 608.5; DB 9; Length 378;
Best Local Similarity 36.9%; Pred. No. 1,1e-43;

Matches 122; Conservative 84; Mismatches 106; Indels 19; Gaps 8;

QY 24 QDFLQFSKVFLLPCMYLVFVCGVLSVLYISIEFHKLQSLDVLVNLPLADLVFVCT 83
DB 51 KDVANFRKAMPLPIWYSIICEVGLGNGLVLYTYFRKLTMDTYLLNLAVADILFLT 110
QY 84 LPEWYAGIHENWFGVGMCKSLGITYINFTYSLITCTVDFRYVYVATKAYNOQAK 143
DB 111 LPEWYAGIAASWVGVHFCILIPATYMSFSGMLLCTSIDRYAIVQAVSAHRRAR 170
QY 144 RMTWGVTSLLIWLISLVSPQIIGNV---FNLDKLICGY--HDEAISTVLATQMT 197
DB 171 VLLISKLSGVIWILATVLSIPELTSDDLGRSSSEQAMRSLTHEVEATITQVA-QWY 229
QY 198 LGFFPLTMIVCYSVIIRKLHAGFQKHRSKIIFLVAVVLLQMPEN-----LM 250
DB 230 IGFVLPLAMSFYLVIIIRTLQARNERKRAKIVIAVVVIVFQPLPYNGVLAQYVA 289
QY 251 KF-IRSTHWEYVAMTSFHYTIMVTEAIVLRACTNPVLYAFVSLKFRKNWKLVDIGCL 309
DB 290 NFMTSSTGLSGLQNLNAD--VYSLACYRCVGNPFLAIFGVKFRNDLFLKFDGL 347
QY 310 PYLGVSQHKRSSEDSNKTFSASHNVEATSNF 340
DB 348 SQEQL-RQWSSCR-HIRRSMSVEAEFTTTF 376

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2003, 07:17:25 ; Search time 26 seconds
(without alignments)
387.025 Million cell updates/sec

Title: US-09-940-063-2
Perfect score: 1794
Sequence: 1 MAEDHYHEDGFSSFNDSQ.....DNKTFESASHNEATSMFOL 342

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Indexed: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
1	1794	100.0	342	2	US-08-742-011-2	Sequence 2, Appl
2	1794	100.0	342	4	US-09-275-384B-5	Sequence 5, Appl
3	1794	100.0	342	4	US-09-116-498-2	Sequence 2, Appl
4	1794	100.0	342	4	US-09-449-437A-2	Sequence 2, Appl
5	1730	96.4	342	4	US-09-517-605-9	Sequence 9, Appl
6	1730	96.4	342	4	US-09-116-498-6	Sequence 6, Appl
7	1717	95.7	342	4	US-09-116-498-4	Sequence 4, Appl
8	619	34.5	374	4	US-09-045-583-48	Sequence 48, Appl
9	619	34.5	374	4	US-09-534-185-48	Sequence 48, Appl
10	612	34.1	357	4	US-09-266-464-2	Sequence 2, Appl
11	608.5	33.9	358	3	US-08-153-848-19	Sequence 19, Appl
12	608.5	33.9	358	3	US-09-299-843A-15	Sequence 15, Appl
13	608.5	33.9	358	4	US-09-088-337B-19	Sequence 19, Appl
14	608.5	33.9	358	5	PCT-US93-11153-19	Sequence 19, Appl
15	608.5	33.9	378	1	US-08-153-848-15	Sequence 15, Appl
16	608.5	33.9	378	3	US-09-299-843A-15	Sequence 15, Appl
17	608.5	33.9	378	3	US-09-299-843A-66	Sequence 66, Appl
18	608.5	33.9	378	4	US-09-251-545-1	Sequence 1, Appl
19	608.5	33.9	378	4	US-09-088-337B-15	Sequence 15, Appl
20	608.5	33.9	378	4	US-09-088-337B-66	Sequence 66, Appl
21	608.5	33.9	378	5	PCT-US93-11153-15	Sequence 15, Appl
22	608.5	33.9	410	1	US-08-153-848-7	Sequence 7, Appl
23	608.5	33.9	410	3	US-09-299-843A-7	Sequence 7, Appl
24	608.5	33.9	410	4	US-09-088-337B-7	Sequence 7, Appl
25	608.5	33.9	410	5	PCT-US93-11153-7	Sequence 7, Appl
26	606	33.8	359	1	US-08-153-848-24	Sequence 24, Appl
27	606	33.8	359	3	US-09-299-843A-24	Sequence 24, Appl

28	606	33.8	359	4	US-09-088-337B-24	Sequence 24, Appl
29	606	33.8	359	5	PCT-US93-11153-24	Sequence 24, Appl
30	588.5	32.8	378	1	US-08-383-750-2	Sequence 2, Appl
31	588.5	32.8	378	1	US-08-383-751A-2	Sequence 2, Appl
32	588.5	32.8	378	3	US-08-352-678-2	Sequence 2, Appl
33	588.5	32.8	378	4	US-09-045-583-49	Sequence 49, Appl
34	588.5	32.8	378	5	US-09-534-185-49	Sequence 49, Appl
35	588.5	32.8	378	5	PCT-US93-09636-2	Sequence 2, Appl
36	568	31.7	350	2	US-08-966-316-18	Sequence 18, Appl
37	560	31.2	350	2	US-08-966-316-16	Sequence 16, Appl
38	554	30.9	361	2	US-08-902-294-2	Sequence 2, Appl
39	554	30.9	361	3	US-09-178-637-2	Sequence 2, Appl
40	527.5	29.4	360	4	US-08-833-752-7	Sequence 7, Appl
41	524.5	29.2	352	1	US-08-202-056-3	Sequence 3, Appl
42	524.5	29.2	352	1	US-08-076-093A-4	Sequence 4, Appl
43	524.5	29.2	352	1	US-08-701-265-4	Sequence 4, Appl
44	524.5	29.2	352	2	US-08-284-586-4	Sequence 4, Appl
45	524.5	29.2	352	2	US-08-805-478-4	Sequence 4, Appl

ALIGNMENTS

```
RESULT 1
US-08-742-011-2
: Sequence 2, Application US/08742011
: Patent No. 5824504
:
GENERAL INFORMATION:
: APPLICANT: Elshourbagy, Nabil A.
: APPLICANT: Bergsma, Dirk J.
: APPLICANT: Ellis, Catherine E.
: TITLE OF INVENTION: Human 7-Transmembrane Receptor
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESSES:
: ADDRESS: Smithline Beecham Corporation
: STREET: 709 Swedeland Road
: CITY: King of Prussia
: STATE: Pennsylvania
: COUNTRY: USA
: ZIP: 19406-2799
:
COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
:
CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/742,011
: FILING DATE:
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: Han, William T.
: REGISTRATION NUMBER: 34,344
: REFERENCE/DOCKET NUMBER: ATG50020P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 610-270-5090
: TELEFAX: 610-270-5219
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 342 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-742-011-2
:
Query Match      100.0%; Score 1794; DB 2; Length 342;
Best Local Similarity 100.0%; Pred. No. 1,6e-142;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 1 MAEDHYHEDGFSSFNDSQOEHDPLQFSCVPLPCMYLVFVCGLVGNSLVLTSTFYH 60
DB 1 MAEDHYHEDGFSSFNDSQOEHDPLQFSCVPLPCMYLVFVCGLVGNSLVLTSTFYH 60
OY 61 KLSGLTDFVLNPLADLVFVCTLPFWAYAGIHBEWFGQWCKSLGITYINFTSMIL 120

Db 61 KLSLTDVFLVNLPLADLVFVCTLPFWAGIHEWFGVGMCKSLIGITINFTSMIL 120
QY 121 TCITVDFRIVVAKATKAYNOAKRMWGVISLLIMVISLVSIPQIITGVNPNLKLIC 180
Db 121 TCITVDFRIVVAKATKAYNOAKRMWGVISLLIMVISLVSIPQIITGVNPNLKLIC 180
QY 181 GYHDEAISTVLAOTMTLGFPLPLMTIYCVSVIITKLLHAGGFKHRSKIIIFLVMAVF 240
Db 181 GYHDEAISTVLAOTMTLGFPLPLMTIYCVSVIITKLLHAGGFKHRSKIIIFLVMAVF 240
QY 241 LITOMPENLMKFIIRSTHMEYAMTSFHYTIMVTEAIAVLRACLNPLVLAFAVSLKFRKNFW 300
Db 241 LITOMPENLMKFIIRSTHMEYAMTSFHYTIMVTEAIAVLRACLNPLVLAFAVSLKFRKNFW 300
QY 301 KLVKDIGCLPYLGVSHQWKSSEDNSKTFSSASHNEATSMFOL 342
Db 301 KLVKDIGCLPYLGVSHQWKSSEDNSKTFSSASHNEATSMFOL 342

RESULT 2
Sequence 5, Application US/09275384B
Patent No. 6232084
GENERAL INFORMATION:
APPLICANT: MACPHEE, COLIN HOUSTON
APPLICANT: MOORES, KITTY
TITLE OF INVENTION: NEW USE
FILE REFERENCE: GH-31106
CURRENT APPLICATION NUMBER: US/09/275.384B
CURRENT FILING DATE: 1999-03-24
PRIOR APPLICATION NUMBER: 9806677.2
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 342
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-275-384B-5

Query Match 100.0%; Score 1794; DB 4; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.6e-142;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAEHDYHEDYGFSSFNDSOEHDQLOFSKVFLPCMYLVFVCGLVGNSLVVISIFYH 60
Db 1 MAEHDYHEDYGFSSFNDSOEHDQLOFSKVFLPCMYLVFVCGLVGNSLVVISIFYH 60
QY 61 KLSLTDVFLVNLPLADLVFVCTLPFWAGIHEWFGVGMCKSLIGITINFTSMIL 120
Db 61 KLSLTDVFLVNLPLADLVFVCTLPFWAGIHEWFGVGMCKSLIGITINFTSMIL 120
QY 121 TCITVDFRIVVAKATKAYNOAKRMWGVISLLIMVISLVSIPQIITGVNPNLKLIC 180
Db 121 TCITVDFRIVVAKATKAYNOAKRMWGVISLLIMVISLVSIPQIITGVNPNLKLIC 180
QY 181 GYHDEAISTVLAOTMTLGFPLPLMTIYCVSVIITKLLHAGGFKHRSKIIIFLVMAVF 240
Db 181 GYHDEAISTVLAOTMTLGFPLPLMTIYCVSVIITKLLHAGGFKHRSKIIIFLVMAVF 240
QY 241 LITOMPENLMKFIIRSTHMEYAMTSFHYTIMVTEAIAVLRACLNPLVLAFAVSLKFRKNFW 300
Db 241 LITOMPENLMKFIIRSTHMEYAMTSFHYTIMVTEAIAVLRACLNPLVLAFAVSLKFRKNFW 300
QY 301 KLVKDIGCLPYLGVSHQWKSSEDNSKTFSSASHNEATSMFOL 342
Db 301 KLVKDIGCLPYLGVSHQWKSSEDNSKTFSSASHNEATSMFOL 342

Patent No. 6251582
GENERAL INFORMATION:
Applicant: Littman, Dan R.
Deng, Hongkui
Unutmaz, Derya
Ramani, Vineet N.K.
TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF
IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USE
THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESS: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116.498
FILING DATE: 16-Jul-1998
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-116-498-2
Query Match 100.0%; Score 1794; DB 4; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.6e-142;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAEHDYHEDYGFSSFNDSOEHDQLOFSKVFLPCMYLVFVCGLVGNSLVVISIFYH 60
Db 1 MAEHDYHEDYGFSSFNDSOEHDQLOFSKVFLPCMYLVFVCGLVGNSLVVISIFYH 60
QY 61 KLSLTDVFLVNLPLADLVFVCTLPFWAGIHEWFGVGMCKSLIGITINFTSMIL 120
Db 61 KLSLTDVFLVNLPLADLVFVCTLPFWAGIHEWFGVGMCKSLIGITINFTSMIL 120
QY 121 TCITVDFRIVVAKATKAYNOAKRMWGVISLLIMVISLVSIPQIITGVNPNLKLIC 180
Db 121 TCITVDFRIVVAKATKAYNOAKRMWGVISLLIMVISLVSIPQIITGVNPNLKLIC 180
QY 181 GYHDEAISTVLAOTMTLGFPLPLMTIYCVSVIITKLLHAGGFKHRSKIIIFLVMAVF 240
Db 181 GYHDEAISTVLAOTMTLGFPLPLMTIYCVSVIITKLLHAGGFKHRSKIIIFLVMAVF 240
QY 241 LITOMPENLMKFIIRSTHMEYAMTSFHYTIMVTEAIAVLRACLNPLVLAFAVSLKFRKNFW 300
Db 241 LITOMPENLMKFIIRSTHMEYAMTSFHYTIMVTEAIAVLRACLNPLVLAFAVSLKFRKNFW 300
QY 301 KLVKDIGCLPYLGVSHQWKSSEDNSKTFSSASHNEATSMFOL 342
Db 301 KLVKDIGCLPYLGVSHQWKSSEDNSKTFSSASHNEATSMFOL 342

Db 301 KLVKDIGCLPYLGVSHPKSSSEDSKTFSSASHNEATSMFOL 342

RESULT 4
US-09-449-437A-2

Sequence 2, Application US/09449437A
Patent No. 6319675
GENERAL INFORMATION:
APPLICANT: Briskin, Michael J.
APPLICANT: Murphy, Kristine E.
APPLICANT: Wilbanks, Alyson M.
APPLICANT: Wu, Lijun
TITLE OF INVENTION: No. 6319675el Antibodies and Ligands for "Bonzo"
FILE REFERENCE: 1855.1070-000
CURRENT APPLICATION NUMBER: US/09/449,437A
CURRENT FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 342
TYPE: PRT
ORGANISM: Homo sapiens
US-09-449-437A-2

Query Match 100.0%; Score 1794; DB 4; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.6e-142;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEHYHEDYGFSSFNDSOEHODFLOFSKVFPLPCMYLVFVCGVGNLSLVISIFYH 60
1 MAEHYHEDYGFSSFNDSOEHODFLOFSKVFPLPCMYLVFVCGVGNLSLVISIFYH 60
Db 1 MAEHYHEDYGFSSFNDSOEHODFLOFSKVFPLPCMYLVFVCGVGNLSLVISIFYH 60
QY 61 KLGSLTFVFLNPLADLVFCTLPFMAAGIHHEWVGQVCKSLGIYTFNFTSMIL 120
61 KLGSLTFVFLNPLADLVFCTLPFMAAGIHHEWVGQVCKSLGIYTFNFTSMIL 120
Db 61 KLGSLTFVFLNPLADLVFCTLPFMAAGIHHEWVGQVCKSLGIYTFNFTSMIL 120
QY 121 TCITVDFRIVVKKATKAYNOQAKRMWGKVTSLIWIISLVSLPQIITYGVNFDKILIC 180
121 TCITVDFRIVVKKATKAYNOQAKRMWGKVTSLIWIISLVSLPQIITYGVNFDKILIC 180
Db 121 TCITVDFRIVVKKATKAYNOQAKRMWGKVTSLIWIISLVSLPQIITYGVNFDKILIC 180
QY 181 GYHDEAISTVVLATQMTLGFPLPLTMIVCSVITIKTLHAGGQKHSKTIIFLVMAVF 240
181 GYHDEAISTVVLATQMTLGFPLPLTMIVCSVITIKTLHAGGQKHSKTIIFLVMAVF 240
Db 181 GYHDEAISTVVLATQMTLGFPLPLTMIVCSVITIKTLHAGGQKHSKTIIFLVMAVF 240
QY 241 LITQMPFNLMKFIRSTHWEYAMTSFHTITVTEAIAVLRACLPVLYAFVSLKFRKNFW 300
241 LITQMPFNLMKFIRSTHWEYAMTSFHTITVTEAIAVLRACLPVLYAFVSLKFRKNFW 300
Db 241 LITQMPFNLMKFIRSTHWEYAMTSFHTITVTEAIAVLRACLPVLYAFVSLKFRKNFW 300
QY 301 KLVKDIGCLPYLGVSHPKSSSEDSKTFSSASHNEATSMFOL 342
301 KLVKDIGCLPYLGVSHPKSSSEDSKTFSSASHNEATSMFOL 342
Db 301 KLVKDIGCLPYLGVSHPKSSSEDSKTFSSASHNEATSMFOL 342

RESULT 5
US-09-517-605-9
Sequence 9, Application US/09517605
Patent No. 6319675
GENERAL INFORMATION:
APPLICANT: Littman, Dan R.
APPLICANT: Kwon, Douglas S.
APPLICANT: van Kooyk, Yvette
APPLICANT: Geiltenbeck, Theo
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
FILE REFERENCE: 1049-1-017
CURRENT APPLICATION NUMBER: US/09/517,605
CURRENT FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 342

TYPE: PRT
ORGANISM: Homo sapiens
US-09-517-605-9

Query Match 100.0%; Score 1794; DB 4; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.6e-142;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEHYHEDYGFSSFNDSOEHODFLOFSKVFPLPCMYLVFVCGVGNLSLVISIFYH 60
1 MAEHYHEDYGFSSFNDSOEHODFLOFSKVFPLPCMYLVFVCGVGNLSLVISIFYH 60
Db 1 MAEHYHEDYGFSSFNDSOEHODFLOFSKVFPLPCMYLVFVCGVGNLSLVISIFYH 60
QY 61 KLGSLTFVFLNPLADLVFCTLPFMAAGIHHEWVGQVCKSLGIYTFNFTSMIL 120
61 KLGSLTFVFLNPLADLVFCTLPFMAAGIHHEWVGQVCKSLGIYTFNFTSMIL 120
Db 61 KLGSLTFVFLNPLADLVFCTLPFMAAGIHHEWVGQVCKSLGIYTFNFTSMIL 120
QY 121 TCITVDFRIVVKKATKAYNOQAKRMWGKVTSLIWIISLVSLPQIITYGVNFDKILIC 180
121 TCITVDFRIVVKKATKAYNOQAKRMWGKVTSLIWIISLVSLPQIITYGVNFDKILIC 180
Db 121 TCITVDFRIVVKKATKAYNOQAKRMWGKVTSLIWIISLVSLPQIITYGVNFDKILIC 180
QY 181 GYHDEAISTVVLATQMTLGFPLPLTMIVCSVITIKTLHAGGQKHSKTIIFLVMAVF 240
181 GYHDEAISTVVLATQMTLGFPLPLTMIVCSVITIKTLHAGGQKHSKTIIFLVMAVF 240
Db 181 GYHDEAISTVVLATQMTLGFPLPLTMIVCSVITIKTLHAGGQKHSKTIIFLVMAVF 240
QY 241 LITQMPFNLMKFIRSTHWEYAMTSFHTITVTEAIAVLRACLPVLYAFVSLKFRKNFW 300
241 LITQMPFNLMKFIRSTHWEYAMTSFHTITVTEAIAVLRACLPVLYAFVSLKFRKNFW 300
Db 241 LITQMPFNLMKFIRSTHWEYAMTSFHTITVTEAIAVLRACLPVLYAFVSLKFRKNFW 300
QY 301 KLVKDIGCLPYLGVSHPKSSSEDSKTFSSASHNEATSMFOL 342
301 KLVKDIGCLPYLGVSHPKSSSEDSKTFSSASHNEATSMFOL 342
Db 301 KLVKDIGCLPYLGVSHPKSSSEDSKTFSSASHNEATSMFOL 342

RESULT 6
US-09-116-498-6
Sequence 6, Application US/09116498
Patent No. 6251582
GENERAL INFORMATION:
APPLICANT: Littman, Dan R.
Deng, Hongkui
Unutmaz, Derya
Ramani, Vineet N.K.
TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF
IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USE
THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116,498
FILING DATE: 16-Jul-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

```

:
: LENGTH: 342 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHETICAL: NO
: ORIGINAL SOURCE:
: ORGANISM: pigtail macaque
: SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-116-498-6

Query Match          96.4%: Score 1730; DB 4; Length 342;
Best Local Similarity 95.6%: Pred. No. 3.6e-137;
Matches 327; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAEHYHEDYGFSSFNDSOEHDPLQFSKVFPLPCMYLVVFGGLVNSLVYISIFH 60
D 1 MAEHYHEDYGLNFSNDSOEHDPLQFRKVFPLPCMYLVVFGGLVNSLVYISIFH 60
QY 61 KLSLTDVFLVNLPLADLVFVCTLPFWAAGIHEWVGQVCKSLGIYITNFTSMIL 120
D 61 KLSLTDVFLVNLPLADLVFVCTLPFWAAGIHEWVGQVCKSLGIYITNFTSMIL 120
QY 121 TCITVDREFIVVVKATKAYNOAKRMWGKYSLLIWIISLVSLPQIITGVNFDKILC 180
D 121 TCITVDREFIVVVKATKAYNOAKRMWGKYSLLIWIISLVSLPQIITGVNFDKILC 180
QY 181 GYHDEASTVLAQTMLGFFLLTMIVCYSVIITKTLHAGFGQKRSKIIFLVAVF 240
D 181 GYHDEASTVLAQTMLGFFLLTMIVCYSVIITKTLHAGFGQKRSKIIFLVAVF 240
QY 241 LTQMPNLMKFRSTHWEYAMTSFHYITIMVTAIYLRACLPVLYAFVSLKFRNFW 300
D 241 LTQMPNLMKFRSTHWEYAMTSFHYITIMVTAIYLRACLPVLYAFVSLKFRNFW 300
QY 301 KLVNDIGCLPYLGSHQKSESDSKTFSSASHNEATSMFOL 342
D 301 KLVNDIGCLPYLGSHQKSESDSKTFSSASHNEATSMFOL 342

RESULT 7
US-09-116-498-4
: Sequence 4, Application US/09116498
: Patent No. 6251582
: GENERAL INFORMATION:
: APPLICANT: Littman, Dan R.
: Deng, Hongkui
: Unutmaz, Derya
: Ramani, Vineet N.K.
: TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
: ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF
: IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES
: THEREOF
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: David A. Jackson, Esq.
: STREET: 411 Hackensack Ave, Continental Plaza, 4th
: Floor
: CITY: Hackensack
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/116,498
: FILING DATE: 16-Jul-1998
: CLASSIFICATION: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Jackson Esq., David A.
```

```

:
: REGISTRATION NUMBER: 26,742
: REFERENCE/DOCKET NUMBER: 1049-1-009
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-487-5800
: TELEFAX: 201-343-1684
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 342 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHETICAL: NO
: ORIGINAL SOURCE:
: ORGANISM: African Green Monkey
: SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-116-498-4

Query Match          95.7%: Score 1717; DB 4; Length 342;
Best Local Similarity 95.3%: Pred. No. 4.4e-136;
Matches 326; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAEHYHEDYGFSSFNDSOEHDPLQFSKVFPLPCMYLVVFGGLVNSLVYISIFH 60
D 1 MAEHYHEDYGLNFSNDSOEHDPLQFSKVFPLPCMYLVVFGGLVNSLVYISIFH 60
QY 61 KLSLTDVFLVNLPLADLVFVCTLPFWAAGIHEWVGQVCKSLGIYITNFTSMIL 120
D 61 KLSLTDVFLVNLPLADLVFVCTLPFWAAGIHEWVGQVCKSLGIYITNFTSMIL 120
QY 121 TCITVDREFIVVVKATKAYNOAKRMWGKYSLLIWIISLVSLPQIITGVNFDKILC 180
D 121 TCITVDREFIVVVKATKAYNOAKRMWGKYSLLIWIISLVSLPQIITGVNFDKILC 180
QY 181 GYHDEASTVLAQTMLGFFLLTMIVCYSVIITKTLHAGFGQKRSKIIFLVAVF 240
D 181 GYHDEASTVLAQTMLGFFLLTMIVCYSVIITKTLHAGFGQKRSKIIFLVAVF 240
QY 241 LTQMPNLMKFRSTHWEYAMTSFHYITIMVTAIYLRACLPVLYAFVSLKFRNFW 300
D 241 LTQMPNLMKFRSTHWEYAMTSFHYITIMVTAIYLRACLPVLYAFVSLKFRNFW 300
QY 301 KLVNDIGCLPYLGSHQKSESDSKTFSSASHNEATSMFOL 342
D 301 KLVNDIGCLPYLGSHQKSESDSKTFSSASHNEATSMFOL 342

RESULT 8
US-09-045-583-48
: Sequence 48, Application US/09045583
: Patent No. 6287805
: GENERAL INFORMATION:
: APPLICANT: Graham, Gerard J. et al.
: TITLE OF INVENTION: NO. 6287805el Molecules of the G Protein-Coupled
: NUMBER OF SEQUENCES: 56
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LAHIVE & COCKFIELD, LLP
: STREET: 28 State Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/045,583
: FILING DATE: 20-MAR-98
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
```



```

APPLICATION NUMBER: US/09/534, 185
FILING DATE: 24-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045, 583
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNT-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-534-185-48

Query Match      34.5%; Score 619; DB 4; Length 374;
Best Local Similarity 36.3%; Pred. No. 2,2e-44;
Matches 135; Conservative 77; Mismatches 116; Indels 44; Gaps 9

QY 5 DYHEDYGSSFNDSQGEHODEL-----QFSKVFPLQWYLVFVCGIYVGNLSIYLVIS 56
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 13 DSSEDY-FVSVNTSYYSVDSEKLLCSLQDEVRQSFLEVPVIAISLVCPELLGNILVITF 71
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 57 IFEYKLSLTQVFLVFLNEPLADLVFVCTLPFWAYA-GIHEWVGQWCKSLGIYITNEYT 115
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 72 AFYKARSMTDYVLLNMAIDILFVLLPEMAVSHATGAWVESNATCKLKGAIYAINFNC 131
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 116 SMLLTCTTVRFPIYVAVATKAYNOQAKRMWGKVTSLIIVISILSVISLPQIIYGVNVL 175
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 132 GMLLTCTISMRYIAIVQATKRSFRLRSRTLPRSKITCIYVWGLSVIISSTVFQNKYMT 191
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 176 D-KLTCGHDAIS-----FVVLATQMTLGFELPLTMIVCYSVIYIKLLHAGGQKRR 228
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 192 QGSDVCEPKRYTQVSEPIRWKLLMLGLLELFGFIFLMPIRFTYIVTKLVQAQNSKRK 251
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 229 SLKTIFLVAVFLLTQMPENL-----KFIKSTHWEYYAMTSFHYITVTEAIAYL 279
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 252 AIRVIAVAVLELQCIPIHNNVLVTAAANLGKMNKSCSE---KLIGYTKIVTEVLAFL 307
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 280 RACINPVIYXAVSLKFRKNFKIYVADICPLPLGYSHQMS-----SDNSKTFESA 330
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 308 HCCINPVIYATIGQAFNNYFLKILKDLWC---VRRYKSSGFSQAGRYSENISRQISE 362
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 331 SHNVEATSMFQL 342
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 363 TADNDNASSFTM 374
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 10
US-09-266-464-2
Sequence 2, Application US/09266464
GENERAL INFORMATION:
APPLICANT: Andrew, David P.
APPLICANT: Zabel, Brian A.
APPLICANT: Ponath, Paul D.
TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
FILE REFERENCE: LKS98-16
TITLE OF INVENTION: IDENTIFYING AGENTS WHICH MODULE GPR-9-6 FUNCTION
CURRENT APPLICATION NUMBER: US/09/266,464
CURRENT FILING DATE: 1999-03-11
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 357
TYPE: PRT

```


US-09-088-337B-19

Query Match	33.9%	Score 608.5	DB 4	Length 358;
Best Local Similarity	36.9%	Pred. No. 1.6e-43		
Matches 122; Conservative	84;	Mismatches 106;	Indels 19;	Gaps 8

```

24 QDPLQFSKYLEPCMLVFWCGLGNSLNLVLSIFVHKQSLTDVFLNPLADLAVFCT 83
      :| | | | : | | | | : : : : | : | : | : | : | : | : |
Db 31 KDVRNFKAMEFLPIMSIICFVGLGSLGVLVLTYYIFKRKLKMTDTYILNLAVADILEFLT 90

```

QY 84 LPFNAAYAGHEWVFGQVMCKSLGITYTINFTSMILLCITVDREFIVVKATKAIYNQAK 1433

Db 91 LPFNAYSAAKSWVEGVHFCKLIFATLYKMSFFSGMELDLCLSIDRYAIVQAASAHRRHAR 1500

```
QY      144 RMFMGKVTSLTIWVLSLVSLLPQIIYGNV---FNIDKLIGY--HDEAISTVLAHQMT 197
      : |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      151 VLLISKLSCGVIMLIVATVLSIPELLYSDLQRSSSEQAMRCLITEHYEAFITQVA-QMV 209
```

```
QY      198 LGFFPLMLIVCYSVIIKTLTHAGSGFQKHRSKLIFLVMVAFLLTQMPFN-----LM 250G
       :|::||| | ||:||||| | :::::::| |::|::|:|
Db      210 IGLVPLLMSCFLVIIRLLQARNEERNAIKIIVAVVFIVEQLPYNGVLAOIVA 269NVS
```

Qy 251 KF-IRSTHMEYYAMTSFHYITWTEAIALACLAENVLYALVSLKPKKNFMVLKVDIGCL 309

Db 270 NFNTSSITCELSKOLNIAYD--VYVSLACVRCVNPFLYATIGVKPRNDLKRFLKDGCL 327

GENERAL INFORMATION:

APPLICANT: Godiska, Ronald

Gray, Patrick W

TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors

CORRESPONDENCE ADDRESS:

Börün

CITY: Chicago

COUNTRY: USA

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

SOFTWARE: Patent In Release #1 0. Version #1 25

APPLICATION DATA:
APPLICATION NUMBER: ITS/09/088 337B

FILING DATE: 01-JUN-1998
 CLASSIFICATION: <Unkown>

PRIOR APPLICATION DATA: HC 08/1E3 848

FILED DATE: 11-NOV-1993

```

1      FILING DATE: 17-NOV-1992
2
3      ATTORNEY/AGENT INFORMATION:
4          NAME: No. 634857and, Greta E.
5          REGISTRATION NUMBER: 35,302
6          REFERENCE/DOCKET NUMBER: 31794
7      TELECOMMUNICATION INFORMATION:
8          TELEPHONE: (312) 474-6300
9          TELEFAX: (312) 474-0448
10         TELEX: 253856
11
12     INFORMATION FOR SEQ ID NO: 19:
13         SEQUENCE CHARACTERISTICS:
14             LENGTH: 358 amino acids
15             TYPE: amino acid
16             TOPOLOGY: linear
17     MOLECULE TYPE: protein
18     SEQUENCE DESCRIPTION: SEQ ID NO: 19:
19
20     US-09-088-337B-19
21
22     Query Match          33.9%; Score 608.5; DB 4; Length 358;
23     Best Local Similarity 36.9%; Pred. No. 1,6e-43;
24     Matches 122; Conservative 84; Mismatches 106; Indels 19; Gaps 8
25
26     QY 24 QDFOGKSVFLPCMTLVVFCVGLGNSLVLYISIFYHKLQSLTDVLYNPLADLVFCT 83
27         : 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
28         31 KDVNFRKMFPLPIWYSIIICFGLGDLGNGLVLYLYFKRLKMTDLYLLNLVADLLFLYT 90
29
30     QY 84 LPEAAVGIHEDVWGVQVNCSTSLGIYTIINFTSMILICIFYDRFIYVAKTKAVNOAK 143
31         LPEAAVGIHEDVWGVQVNCSTSLGIYTIINFTSMILICIFYDRFIYVAKTKAVNOAK 143
32         91 LPEAAVSAKSWGVGVHPCCKLIFATYKNSFFSGMLLLCISIDRIYVAIVQAVSAHRHRAR 150
33
34     QY 144 RMTGKATVSLTIWYISLAVSLDPIIYGNV---FNLDKLCIGY--HDEAISTVLTATQMT 197
35         : 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
36         151 VLLSKLSCVGMILAVTLATVSLPELLYSLDLOKSSSPQARCSLTIEHVEAFITGYA-QMV 209
37
38     QY 198 LGFPLPLLTMTVCVSVIITKTLIHAGGPKKHSKTIIELYMAVELLTQMPN-----LM 250
39         : 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
40         210 IGFVLPLPLAMSFCLYVLIITRLQARFNERNNAIKYLIADVVFVIFQLPYNGVLAQTVA 269
41
42     QY 251 KF-IRSTHWEYVAMTSFHYITIMVTEAIVLRACILNPVLYAVSLKFRNFMFLVYDGL 309
43         : 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
44         270 NFNTSTSPICELSKQNLNIAYD-VYPSLACVRCQVNPFLYAFIGVFRNDLFLPLFDGL 327
45
46     QY 310 PYLGVSQHWKSSSDNSKTFSSAHNVEATSMF 340
47         : 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
48         Db 328 SQEQL-RQWSSCR-HIRRSSMSVEAETTTTF 356
49
50     RESULT 14
51     PCT-US93-11153-19
52     Sequence 19, Application PC/TUS93111153
53     GENERAL INFORMATION:
54         APPLICANT: Godiska, Ronald
55         APPLICANT: Gray, Patrick W.
56         APPLICANT: Schweikart, Vicki L.
57     TITLE OF INVENTION: Novel Seven Transmembrane Receptors
58     NUMBER OF SEQUENCES: 64
59     CORRESPONDENCE ADDRESSES:
60         ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
61         ADDRESSEE: Bicknell
62         STREET: 6300 Sears Tower, 233 South Wacker Drive
63         CITY: Chicago
64         STATE: Illinois
65         COUNTRY: USA
66         ZIP: 60606
67     COMPUTER READABLE FORM:
68         MEDIUM TYPE: Floppy disk
69         COMPUTER: IBM PC compatible
70         OPERATING SYSTEM: PC-DOS/MS-DOS
71         SOFTWARE: PatentIn Release #1.0, Version #1.25
72     CURRENT APPLICATION DATA:
73         APPLICATION NUMBER: PCT/US93/11153
74         FILING DATE:
75     CLASSIFICATION:

```

